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<110> Evolutionary Genomics LLC
<120> Development of Therapeutics for the Treatment of Endotoxin-Mediated Diseases
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<150> 10/100,422
<151> 2002-03-18
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Leu	Gln	Val	Leu	Asp	Leu	Ser	Arg	Cys	Glu	Ile	Gln	Thr	Ile	Glu	Asp	
				50			55		60							
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Gly	Ala	Tyr	Gln	Ser	Leu	Ser	His	Leu	Ser	Thr	Leu	Ile	Leu	Thr	Gly	
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Asn	Pro	Ile	Gln	Ser	Leu	Ala	Leu	Gly	Ala	Phe	Ser	Gly	Leu	Ser	Ser	
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Asn Pro Ile Gln Ser Leu Ala Leu Gly Ala Phe Ser Gly Leu Ser Ser
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Leu Gln Lys Leu Val Ala Val Glu Thr Asn Leu Ala Ser Leu Glu Asn
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Phe Pro Ile Gly His Leu Lys Thr Leu Lys Glu Leu Asn Val Ala His
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Asn Leu Glu Tyr Leu Asp Leu Ser Ser Asn Lys Ile Gln Ser Ile Tyr
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Cys Thr Asp Leu Arg Val Leu His Gln Met Pro Leu Leu Asn Leu Ser
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Lys Glu Ile Arg Leu His Lys Leu Thr Leu Arg Asn Asn Phe Asp Ser
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Phe Asp Lys Ser Ala Leu Glu Gly Leu Cys Asn Leu Thr Ile Glu Glu
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Phe Arg Leu Ala Tyr Leu Asp Tyr Tyr Leu Asp Asp Ile Ile Asp Leu
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Phe Asn Cys Leu Thr Asn Val Ser Ser Phe Ser Leu Val Ser Val Thr
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Ser Asn Phe Leu Gly Leu Glu Gln Leu Glu His Leu Asp Phe Gln His
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Ser Pro Thr Ala Phe Asn Ser Leu Ser Ser Leu Gln Val Leu Asn Met
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Ser His Asn Asn Phe Phe Ser Leu Asp Thr Phe Pro Tyr Lys Cys Leu
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Asn Ser Leu Arg Val Leu Asp Tyr Ser Leu Asn His Ile Met Thr Ser
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Lys Lys Gln Glu Leu Gln His Phe Pro Ser Ser Leu Ala Phe Leu Asn
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Leu Thr Gln Asn Asp Phe Ala Cys Thr Cys Glu His Gln Ser Phe Leu
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Gln Trp Ile Lys Asp Gln Arg Gln Leu Leu Val Glu Val Glu Arg Met
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Glu Cys Ala Thr Pro Ser Asp Lys Gln Gly Met Pro Val Leu Ser Leu
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Phe His Leu Met Leu Leu Ala Gly Cys Ile Lys Tyr Gly Arg Gly Glu
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Ala Asn Ile Ile His Glu Gly Phe His Lys Ser Arg Lys Val Ile Val
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ttt cac ctg atg ctt ctt gct ggc tgc atg aag tat ggt aga ggt gaa Phe His Leu Met Leu Leu Ala Gly Cys Met Lys Tyr Gly Arg Gly Glu 625 630 635 640	1920
aac acc tat gat gcc ttt gtt atc tac tcc agc cag gat gag gac tgg Asn Thr Tyr Asp Ala Phe Val Ile Tyr Ser Ser Gln Asp Glu Asp Trp 645 650 655	1968
gta agg aat gag cta gta aag aat tta gaa gaa ggg gtg cct ccc ttt Val Arg Asn Glu Leu Val Lys Asn Leu Glu Glu Gly Val Pro Pro Phe 660 665 670	2016

cag ctc tgc ctt cac tac aga gac ttt att ccy ggt gtg gcc att gct Gln Leu Cys Leu His Tyr Arg Asp Phe Ile Xaa Gly Val Ala Ile Ala 675 680 685	2064
gcc aac atc atc cat gaa ggt ttc cat aaa agc cga aag gtg att gtt Ala Asn Ile Ile His Glu Gly Phe His Lys Ser Arg Lys Val Ile Val 690 695 700	2112
gtg gtg tcc cag cac ttc atc cag agc cgc tgg tgt atc ttt gag tat Val Val Ser Gln His Phe Ile Gln Ser Arg Trp Cys Ile Phe Glu Tyr 705 710 715 720	2160
gag att gct cag acc tgg cag ttt ctg agc agt cat gct ggg atc atc Glu Ile Ala Gln Thr Trp Gln Phe Leu Ser Ser His Ala Gly Ile Ile 725 730 735	2208
ttc att gtc ctg cag aag gtg gag aag acc ctg ctc agg cag cag gtg Phe Ile Val Leu Gln Lys Val Glu Lys Thr Leu Leu Arg Gln Gln Val 740 745 750	2256
gag ctg tac cgc ctt ctc agc agg aac act tac ctg gag tgg gag gat Glu Leu Tyr Arg Leu Leu Ser Arg Asn Thr Tyr Leu Glu Trp Glu Asp 755 760 765	2304
agt gtc ctg ggg cg ^g cac att ttc tgg aga cga ctc aga aaa gcc ctg Ser Val Leu Gly Arg His Ile Phe Trp Arg Arg Leu Arg Lys Ala Leu 770 775 780	2352
ctg gat ggt aaa tca tgg aat cca gaa gga aca gtg ggt aca gga tgc Leu Asp Gly Lys Ser Trp Asn Pro Glu Gly Thr Val Gly Thr Gly Cys 785 790 795 800	2400
aat tag Asn	2406

<210> 9

<211> 801

<212> PRT

<213> Hylobates lar

<220>

<221> misc_feature

<222> (198)..(198)

<223> The 'Xaa' at location 198 stands for Arg, or His.

<220>

<221> misc_feature

<222> (683)..(683)

<223> The 'Xaa' at location 683 stands for Pro.

<400> 9

Val Val Pro Asn Ile Thr Tyr Gln Cys Met Glu Leu Asn Phe Tyr Lys 1 5 10 15
--

Ile Pro Asp Asn Leu Pro Phe Ser Thr Lys Asn Leu Asp Leu Ser Phe
20 25 30

Asn Pro Leu Arg His Leu Gly Ser Tyr Ser Phe Phe Ser Phe Pro Glu
35 40 45

Leu Gln Val Leu Asp Leu Ser Arg Cys Glu Ile Gln Thr Ile Glu Asp
50 55 60

Gly Ala Tyr Gln Ser Leu Ser Leu Leu Ser Thr Leu Ile Leu Thr Gly
65 70 75 80

Asn Pro Ile Gln Ser Leu Ala Leu Gly Ala Phe Ser Gly Leu Ser Ser
85 90 95

Leu Gln Lys Leu Val Ala Val Glu Thr Asn Leu Ala Ser Leu Glu Asn
100 105 110

Phe Pro Ile Gly His Leu Lys Thr Leu Lys Glu Leu Asn Val Ala His
115 120 125

Asn Leu Ile Gln Ser Phe Lys Leu Pro Glu Tyr Phe Ser Asn Leu Thr
130 135 140

Asn Leu Glu His Leu Asp Leu Ser Ser Asn Lys Ile Gln Ser Ile Tyr
145 150 155 160

Cys Lys Asp Leu Gln Val Leu His Gln Met Pro Leu Leu Asn Leu Ser
165 170 175

Leu Asp Leu Ser Leu Asn Pro Met Asn Phe Ile Gln Pro Gly Ala Phe
180 185 190

Lys Glu Ile Ser Leu Xaa Lys Leu Thr Leu Arg Asn Asn Phe Asp Ser
195 200 205

Leu Asn Val Met Lys Thr Cys Ile Gln Gly Leu Ala Gly Leu Glu Val
210 215 220

His Arg Leu Val Leu Gly Glu Phe Arg Asn Glu Gly Asn Leu Glu Glu
225 230 235 240

Phe Asp Lys Ser Ala Leu Glu Gly Leu Cys Asn Leu Thr Ile Glu Glu
245 250 255

Phe Arg Leu Ala Tyr Leu Asp His Tyr Leu Asp Asp Ile Ile Asp Leu
260 265 270

Phe Asn Cys Leu Ala Asn Val Ser Ser Phe Ser Leu Val Ser Val Thr
275 280 285

Ile Lys Arg Val Glu Asp Phe Ser Tyr Asn Phe Gly Trp Gln His Leu
290 295 300

Glu Leu Val Asn Cys Lys Phe Gly Gln Phe Pro Thr Leu Asn Leu Lys
305 310 315 320

Ser Leu Lys Arg Leu Thr Phe Thr Ala Asn Arg Gly Gly Asn Ala Phe
325 330 335

Ser Glu Val Asp Leu Pro Ser Leu Glu Phe Leu Asp Leu Ser Arg Asn
340 345 350

Gly Leu Ser Phe Lys Gly Cys Cys Ser Gln Ser Asp Phe Gly Thr Asn
355 360 365

Ser Leu Lys Tyr Leu Asp Leu Ser Phe Asn Asp Val Ile Thr Met Ser
370 375 380

Ser Asn Phe Leu Gly Leu Glu Gln Leu Glu His Leu Asp Leu Gln His
385 390 395 400

Ser Asn Leu Lys Gln Met Ser Glu Phe Ser Val Phe Leu Ser Leu Arg
405 410 415

Asn Leu Ile Tyr Leu Asp Ile Ser His Thr His Thr Arg Val Ala Phe
420 425 430

Asn Gly Ile Phe Asn Gly Leu Ser Asn Leu Glu Val Leu Lys Met Ala
435 440 445

Gly Asn Ser Phe Gln Glu Asn Phe Leu Pro Asp Ile Phe Thr Glu Leu
450 455 460

Arg Asn Leu Thr Phe Leu Asp Leu Ser Gln Cys Gln Leu Glu Gln Leu
465 470 475 480

Ser Pro Thr Ala Phe Asn Ser Leu Ser Ser Leu Gln Val Leu Asn Met
485 490 495

Ser His Asn Asn Phe Phe Ser Leu Asp Thr Phe Pro Tyr Lys Cys Leu
500 505 510

Asn Ser Leu Gln Val Leu Asp Tyr Ser Leu Asn His Ile Met Thr Ser
515 520 525

Lys Lys Gln Glu Leu Gln Arg Phe Pro Ser Ser Leu Ala Phe Leu Asn
530 535 540

Leu Thr Gln Asn Asp Phe Ala Cys Thr Cys Glu His Glu Ser Phe Leu
545 550 555 560

Gln Trp Ile Lys Asp Gln Arg Gln Leu Leu Val Glu Val Glu Arg Met
565 570 575

Glu Cys Ala Thr Pro Ser Asp Lys Gln Gly Met Pro Val Leu Ser Leu
580 585 590

Asn Ile Thr Cys Gln Met Asn Lys Thr Ile Ile Gly Val Ser Val Leu
595 600 605

Ser Val Leu Val Val Ser Val Val Ala Val Leu Val Tyr Lys Phe Tyr
610 615 620

Phe His Leu Met Leu Leu Ala Gly Cys Met Lys Tyr Gly Arg Gly Glu
625 630 635 640

Asn Thr Tyr Asp Ala Phe Val Ile Tyr Ser Ser Gln Asp Glu Asp Trp
645 650 655

Val Arg Asn Glu Leu Val Lys Asn Leu Glu Glu Gly Val Pro Pro Phe
660 665 670

Gln Leu Cys Leu His Tyr Arg Asp Phe Ile Xaa Gly Val Ala Ile Ala
675 680 685

Ala Asn Ile Ile His Glu Gly Phe His Lys Ser Arg Lys Val Ile Val
690 695 700

Val Val Ser Gln His Phe Ile Gln Ser Arg Trp Cys Ile Phe Glu Tyr
705 710 715 720

Gly Ile Ala Gln Thr Trp Gln Phe Leu Ser Ser His Ala Gly Ile Ile
725 730 735

Phe Ile Val Leu Gln Lys Val Glu Lys Thr Leu Leu Arg Gln Gln Val
 740 745 750

Glu Leu Tyr Arg Leu Leu Ser Arg Asn Thr Tyr Leu Glu Trp Glu Asp
 755 760 765

Ser Val Leu Gly Arg His Ile Phe Trp Arg Arg Leu Arg Lys Ala Leu
 770 775 780

Leu Asp Gly Lys Ser Trp Asn Pro Glu Gly Thr Val Gly Thr Gly Cys
 785 790 795 800

Asn

<210> 10
 <211> 2388
 <212> DNA
 <213> Macaca mulatta

<400> 10		
gtggttccta atattactta tcaatgcatt gagctgaatt tctacaaaat ccccgacaac		60
ctccccttct caaccaagaa cctggacctg agctttaatc ccctgaggca ttttaggcagc		120
tatagcttct tcagttccc agaactgcag gtgctggatt tatccaggtg taaaatccag		180
acaattgaag atggggcata tcagagccta agccacctct ccacttaat attgacagga		240
aaccccatcc agagtttagc cctgggagcc tttctggac tatcaagttt acagaagctg		300
gtggctgtgg agacaaatct agcatctcta gagaacttcc ccattggaca tctcaaaact		360
ttgaaagaac ttaatgtggc tcacaatctt atccagtctt tcaaattacc tgagtatTTT		420
tctaatctga ccaatctaga gcacttggac cttccagta acaagattca aaatatttat		480
tgcaaagact tgcaggttct acatcaaatg cccctatcca atctctctt agacctgtcc		540
ctgaacccta taaactttat ccaaccaggt gcatttaaag aaatttaggct tcataagctg		600
actttgagaa gtaattttga tgatttaat gtaatgaaaa cttgtattca aggtctggct		660
ggtttagaag tccatcgTTT ggTTCTGGGA gaatttagaa atgaaagaaa cttggaagag		720
tttgacaaat cttctctgga gggattgtgc aatttgcatt ttgaagaatt ccgattaaca		780
tacttagact actacacctga taatattatt gacttattta attgtttggc aaatgtttct		840
tcatTTTCCC tggtgagtgt gagtattaaa aggtagaag acttttctta taatttcaga		900
tggcaacatt tagaatttagt taactgtaaa tttgaacagt ttcccacatt ggaactcgaa		960

tctctcaaaa ggcttacttt cactgccaac aaaggtggga atgcttttc agaagttgat	1020
ctaccaagcc ttgagttct agatctcagt agaaatggct tgagttcaa aggttgctgt	1080
tctcaaagtg attttggac aaccagccta aagtatttag atctgagctt caatgatgtt	1140
attaccatga gttcaaactt cttggccta gaaaaactag aacatctgga tttccagcat	1200
tccaatttga aacagatgag tcaatttca gtattcctat cactcagaaa cctcatttac	1260
cttgacattt ctcatactca caccagagtt gcttcaatg gcatcttcga tggcttgctc	1320
agtctcaaag tcttaaaaat ggctggcaat tcttccagg aaaacttcct tccagatatac	1380
ttcacagatc tgaaaaactt gacccctcg gacccctctc agtgtcaatt ggagcagttg	1440
tctccaacag catggacac actcaacaag cttaggtac taaatatgag ccacaacaac	1500
ttctttcat tggatacgtt tccttataag tgtctgcct ccctccaggt tctcgattac	1560
agtctcaatc acataatgac ttccaacaac caggaactac agcatttcc aagtagtcta	1620
gctttcttaa atcttactca gaatgacttt gcttgtactt gtgaacacca gagttcctg	1680
cagtggatca aggaccagag gcagctctg gtggaaagctg aacgaatgga atgtcaaca	1740
ccttcagata aacagggcat gccggtgctg agttgaata ttacctgtca gatgaataag	1800
accatcattt gtgtgtctgt gttcagtgtg ctgtggtat ctgtgttagc agttctggtc	1860
tataagttct atttcacct gatgcttctt gctggctgca taaastatgg tagaggtgaa	1920
aacatctatg atgccttgt tatctactca agccaggatg aggactgggt aaggaatgaa	1980
ctagtaaaga atttagaaga aggggtgcct cccttcagc tctgccttca ctacagagac	2040
tttattcccg gtgtggccat tgctgcaaac atcatccatg aaggttcca taaaagccga	2100
aaggtgattt ttgtgggtgc ccagcacttc atccagagcc gctgggttat cttgaatat	2160
gagattgctc agacctggca gtttctgagc agtcgtgcag gcataatctt cattgtcctg	2220
cagaaggtgg agaagaccct gctcaggcag caggtggagc tgtaccgcct tctcagcagg	2280
aacacttacc tggagtgaaa ggacagtgtc ctggggcagc acatcttctg gagacgactc	2340
agaaaagccc tggatggatgg cagatcgtgg aatccagaag aacagtag	2388

<210> 11
<211> 2388
<212> DNA
<213> Macaca mulatta

<220>
<221> CDS
<222> (1)..(2388)

<400>	11		
gtg gtt cct aat att act tat caa tgc atg gag ctg aat ttc tac aaa			48
Val Val Pro Asn Ile Thr Tyr Gln Cys Met Glu Leu Asn Phe Tyr Lys			
1	5	10	15
atc ccc gac aac ctc ccc ttc tca acc aag aac ctg gac ctg agc ttt			96
Ile Pro Asp Asn Leu Pro Phe Ser Thr Lys Asn Leu Asp Leu Ser Phe			
20	25	30	
aat ccc ctg agg cat tta ggc agc tat agc ttc ttc agt ttc cca gaa			144
Asn Pro Leu Arg His Leu Gly Ser Tyr Ser Phe Phe Ser Phe Pro Glu			
35	40	45	
ctg cag gtg ctg gat tta tcc agg tgt gaa atc cag aca att gaa gat			192
Leu Gln Val Leu Asp Leu Ser Arg Cys Glu Ile Gln Thr Ile Glu Asp			
50	55	60	
ggg gca tat cag agc cta agc cac ctc tcc act tta ata ttg aca gga			240
Gly Ala Tyr Gln Ser Leu Ser His Leu Ser Thr Leu Ile Leu Thr Gly			
65	70	75	80
aac ccc atc cag agt tta gcc ctg gga gcc ttt tct gga cta tca agt			288
Asn Pro Ile Gln Ser Leu Ala Leu Gly Ala Phe Ser Gly Leu Ser Ser			
85	90	95	
tta cag aag ctg gtg gct gtg gag aca aat cta gca tct cta gag aac			336
Leu Gln Lys Leu Val Ala Val Glu Thr Asn Leu Ala Ser Leu Glu Asn			
100	105	110	
ttc ccc att gga cat ctc aaa act ttg aaa gaa ctt aat gtg gct cac			384
Phe Pro Ile Gly His Leu Lys Thr Leu Lys Glu Leu Asn Val Ala His			
115	120	125	
aat ctt atc cag tct ttc aaa tta cct gag tat ttt tct aat ctg acc			432
Asn Leu Ile Gln Ser Phe Lys Leu Pro Glu Tyr Phe Ser Asn Leu Thr			
130	135	140	
aat cta gag cac ttg gac ctt tcc agt aac aag att caa aat att tat			480
Asn Leu Glu His Leu Asp Leu Ser Ser Asn Lys Ile Gln Asn Ile Tyr			
145	150	155	160
tgc aaa gac ttg cag gtt cta cat caa atg ccc cta tcc aat ctc tct			528
Cys Lys Asp Leu Gln Val Leu His Gln Met Pro Leu Ser Asn Leu Ser			
165	170	175	
tta gac ctg tcc ctg aac cct ata aac ttt atc caa cca ggt gca ttt			576
Leu Asp Leu Ser Leu Asn Pro Ile Asn Phe Ile Gln Pro Gly Ala Phe			
180	185	190	
aaa gaa att agg ctt cat aag ctg act ttg aga agt aat ttt gat gat			624
Lys Glu Ile Arg Leu His Lys Leu Thr Leu Arg Ser Asn Phe Asp Asp			
195	200	205	
tta aat gta atg aaa act tgt att caa ggt ctg gct ggt tta gaa gtc			672
Leu Asn Val Met Lys Thr Cys Ile Gln Gly Leu Ala Gly Leu Glu Val			
210	215	220	
cat cgt ttg gtt ctg gga gaa ttt aga aat gaa aga aac ttg gaa gag			720
His Arg Leu Val Leu Gly Glu Phe Arg Asn Glu Arg Asn Leu Glu Glu			
225	230	235	240

ttt gac aaa tct tct ctg gag gga ttg tgc aat ttg acc att gaa gaa Phe Asp Lys Ser Ser Leu Glu Gly Leu Cys Asn Leu Thr Ile Glu Glu 245 250 255	768
ttc cga tta aca tac tta gac tac tac ctc gat aat att att gac tta Phe Arg Leu Thr Tyr Leu Asp Tyr Tyr Leu Asp Asn Ile Ile Asp Leu 260 265 270	816
ttt aat tgt ttg gca aat gtt tct tca ttt tcc ctg gtg agt gtg agt Phe Asn Cys Leu Ala Asn Val Ser Ser Phe Ser Leu Val Ser Val Ser 275 280 285	864
att aaa agg gta gaa gac ttt tct tat aat ttc aga tgg caa cat tta Ile Lys Arg Val Glu Asp Phe Ser Tyr Asn Phe Arg Trp Gln His Leu 290 295 300	912
gaa tta gtt aac tgt aaa ttt gaa cag ttt ccc aca ttg gaa ctc gaa Glu Leu Val Asn Cys Lys Phe Glu Gln Phe Pro Thr Leu Glu Leu Glu 305 310 315 320	960
tct ctc aaa agg ctt act ttc act gcc aac aaa ggt ggg aat gct ttt Ser Leu Lys Arg Leu Thr Phe Thr Ala Asn Lys Gly Gly Asn Ala Phe 325 330 335	1008
tca gaa gtt gat cta cca agc ctt gag ttt cta gat ctc agt aga aat Ser Glu Val Asp Leu Pro Ser Leu Glu Phe Leu Asp Leu Ser Arg Asn 340 345 350	1056
ggc ttg agt ttc aaa ggt tgc tgt tct caa agt gat ttt ggg aca acc Gly Leu Ser Phe Lys Gly Cys Cys Ser Gln Ser Asp Phe Gly Thr Thr 355 360 365	1104
agc cta aag tat tta gat ctg agc ttc aat gat gtt att acc atg agt Ser Leu Lys Tyr Leu Asp Leu Ser Phe Asn Asp Val Ile Thr Met Ser 370 375 380	1152
tca aac ttc ttg ggc tta gaa aaa cta gaa cat ctg gat ttc cag cat Ser Asn Phe Leu Gly Leu Glu Lys Leu Glu His Leu Asp Phe Gln His 385 390 395 400	1200
tcc aat ttg aaa cag atg agt caa ttt tca gta ttc cta tca ctc aga Ser Asn Leu Lys Gln Met Ser Gln Phe Ser Val Phe Leu Ser Leu Arg 405 410 415	1248
aac ctc att tac ctt gac att tct cat act cac acc aga gtt gct ttc Asn Leu Ile Tyr Leu Asp Ile Ser His Thr His Thr Arg Val Ala Phe 420 425 430	1296
aat ggc atc ttc gat ggc ttg ctc agt ctc aaa gtc tta aaa atg gct Asn Gly Ile Phe Asp Gly Leu Leu Ser Leu Lys Val Leu Lys Met Ala 435 440 445	1344
ggc aat tct ttc cag gaa aac ttc ctt cca gat atc ttc aca gat ctg Gly Asn Ser Phe Gln Glu Asn Phe Leu Pro Asp Ile Phe Thr Asp Leu 450 455 460	1392
aaa aac ttg acc ttc ctg gac ctc tct cag tgt caa ttg gag cag ttg Lys Asn Leu Thr Phe Leu Asp Leu Ser Gln Cys Gln Leu Glu Gln Leu 465 470 475 480	1440

tct cca aca gca ttt gac aca ctc aac aag ctt cag gta cta aat atg Ser Pro Thr Ala Phe Asp Thr Leu Asn Lys Leu Gln Val Leu Asn Met 485 490 495	1488
agc cac aac aac ttc ttt tca ttg gat acg ttt cct tat aag tgt ctg Ser His Asn Asn Phe Phe Ser Leu Asp Thr Phe Pro Tyr Lys Cys Leu 500 505 510	1536
ccc tcc ctc cag gtt ctc gat tac agt ctc aat cac ata atg act tcc Pro Ser Leu Gln Val Leu Asp Tyr Ser Leu Asn His Ile Met Thr Ser 515 520 525	1584
aac aac cag gaa cta cag cat ttt cca agt agt cta gct ttc tta aat Asn Asn Gln Glu Leu Gln His Phe Pro Ser Ser Leu Ala Phe Leu Asn 530 535 540	1632
ctt act cag aat gac ttt gct tgt act tgt gaa cac cag agt ttc ctg Leu Thr Gln Asn Asp Phe Ala Cys Thr Cys Glu His Gln Ser Phe Leu 545 550 555 560	1680
cag tgg atc aag gac cag agg cag ctc ttg gtg gaa gct gaa cga atg Gln Trp Ile Lys Asp Gln Arg Gln Leu Leu Val Glu Ala Glu Arg Met 565 570 575	1728
gaa tgt gca aca cct tca gat aaa cag ggc atg ccg gtg ctg agt ttg Glu Cys Ala Thr Pro Ser Asp Lys Gln Gly Met Pro Val Leu Ser Leu 580 585 590	1776
aat att acc tgt cag atg aat aag acc atc att ggt gtg tct gtg ttc Asn Ile Thr Cys Gln Met Asn Lys Thr Ile Ile Gly Val Ser Val Phe 595 600 605	1824
agt gtg ctt gtg gta tct gtt gta gca gtt ctg gtc tat aag ttc tat Ser Val Leu Val Val Ser Val Val Ala Val Leu Val Tyr Lys Phe Tyr 610 615 620	1872
ttt cac ctg atg ctt ctt gct ggc tgc ata aas tat ggt aga ggt gaa Phe His Leu Met Leu Leu Ala Gly Cys Ile Xaa Tyr Gly Arg Gly Glu 625 630 635 640	1920
aac atc tat gat gcc ttt gtt atc tac tca agc cag gat gag gac tgg Asn Ile Tyr Asp Ala Phe Val Ile Tyr Ser Ser Gln Asp Glu Asp Trp 645 650 655	1968
gta agg aat gaa cta gta aag aat tta gaa gaa ggg gtg cct ccc ttt Val Arg Asn Glu Leu Val Lys Asn Leu Glu Glu Gly Val Pro Pro Phe 660 665 670	2016
cag ctc tgc ctt cac tac aga gac ttt att ccc ggt gtg gcc att gct Gln Leu Cys Leu His Tyr Arg Asp Phe Ile Pro Gly Val Ala Ile Ala 675 680 685	2064
gca aac atc atc cat gaa ggt ttc cat aaa agc cga aag gtg att gtt Ala Asn Ile Ile His Glu Gly Phe His Lys Ser Arg Lys Val Ile Val 690 695 700	2112
gtg gtg tcc cag cac ttc atc cag agc cgc tgg tgt atc ttt gaa tat Val Val Ser Gln His Phe Ile Gln Ser Arg Trp Cys Ile Phe Glu Tyr 705 710 715 720	2160

gag att gct cag acc tgg cag ttt ctg agc agt cgt gca ggc ata atc Glu Ile Ala Gln Thr Trp Gln Phe Leu Ser Ser Arg Ala Gly Ile Ile 725 730 735	2208
ttc att gtc ctg cag aag gtg gag aag acc ctg ctc agg cag cag gtg Phe Ile Val Leu Gln Lys Val Glu Lys Thr Leu Leu Arg Gln Gln Val 740 745 750	2256
gag ctg tac cgc ctt ctc agc agg aac act tac ctg gag tgg gag gac Glu Leu Tyr Arg Leu Leu Ser Arg Asn Thr Tyr Leu Glu Trp Glu Asp 755 760 765	2304
agt gtc ctg ggg cag cac atc ttc tgg aga cga ctc aga aaa gcc ctg Ser Val Leu Gly Gln His Ile Phe Trp Arg Arg Leu Arg Lys Ala Leu 770 775 780	2352
ttg gat ggc aga tcg tgg aat cca gaa gaa cag tag Leu Asp Gly Arg Ser Trp Asn Pro Glu Glu Gln 785 790 795	2388

<210> 12

<211> 795

<212> PRT

<213> Macaca mulatta

<220>

<221> misc_feature

<222> (635)..(635)

<223> The 'Xaa' at location 635 stands for Lys, or Asn.

<400> 12

Val Val Pro Asn Ile Thr Tyr Gln Cys Met Glu Leu Asn Phe Tyr Lys 1 5 10 15
--

Ile Pro Asp Asn Leu Pro Phe Ser Thr Lys Asn Leu Asp Leu Ser Phe 20 25 30

Asn Pro Leu Arg His Leu Gly Ser Tyr Ser Phe Phe Ser Phe Pro Glu 35 40 45

Leu Gln Val Leu Asp Leu Ser Arg Cys Glu Ile Gln Thr Ile Glu Asp 50 55 60

Gly Ala Tyr Gln Ser Leu Ser His Leu Ser Thr Leu Ile Leu Thr Gly 65 70 75 80
--

Asn Pro Ile Gln Ser Leu Ala Leu Gly Ala Phe Ser Gly Leu Ser Ser 85 90 95

Lys Gln Lys Leu Val Ala Val Glu Thr Asn Leu Ala Ser Leu Glu Asn 100 105 110
--

Phe Pro Ile Gly His Leu Lys Thr Leu Lys Glu Leu Asn Val Ala His
115 120 125

Asn Leu Ile Gln Ser Phe Lys Leu Pro Glu Tyr Phe Ser Asn Leu Thr
130 135 140

Asn Leu Glu His Leu Asp Leu Ser Ser Asn Lys Ile Gln Asn Ile Tyr
145 150 155 160

Cys Lys Asp Leu Gln Val Leu His Gln Met Pro Leu Ser Asn Leu Ser
165 170 175

Leu Asp Leu Ser Leu Asn Pro Ile Asn Phe Ile Gln Pro Gly Ala Phe
180 185 190

Lys Glu Ile Arg Leu His Lys Leu Thr Leu Arg Ser Asn Phe Asp Asp
195 200 205

Leu Asn Val Met Lys Thr Cys Ile Gln Gly Leu Ala Gly Leu Glu Val
210 215 220

His Arg Leu Val Leu Gly Glu Phe Arg Asn Glu Arg Asn Leu Glu Glu
225 230 235 240

Phe Asp Lys Ser Ser Leu Glu Gly Leu Cys Asn Leu Thr Ile Glu Glu
245 250 255

Phe Arg Leu Thr Tyr Leu Asp Tyr Tyr Leu Asp Asn Ile Ile Asp Leu
260 265 270

Phe Asn Cys Leu Ala Asn Val Ser Ser Phe Ser Leu Val Ser Val Ser
275 280 285

Ile Lys Arg Val Glu Asp Phe Ser Tyr Asn Phe Arg Trp Gln His Leu
290 295 300

Glu Leu Val Asn Cys Lys Phe Glu Gln Phe Pro Thr Leu Glu Leu Glu
305 310 315 320

Ser Leu Lys Arg Leu Thr Phe Thr Ala Asn Lys Gly Gly Asn Ala Phe
325 330 335

Ser Glu Val Asp Leu Pro Ser Leu Glu Phe Leu Asp Leu Ser Arg Asn
340 345 350

Gly Leu Ser Phe Lys Gly Cys Cys Ser Gln Ser Asp Phe Gly Thr Thr
355 360 365

Ser Leu Lys Tyr Leu Asp Leu Ser Phe Asn Asp Val Ile Thr Met Ser
370 375 380

Ser Asn Phe Leu Gly Leu Glu Lys Leu Glu His Leu Asp Phe Gln His
385 390 395 400

Ser Asn Leu Lys Gln Met Ser Gln Phe Ser Val Phe Leu Ser Leu Arg
405 410 415

Asn Leu Ile Tyr Leu Asp Ile Ser His Thr His Thr Arg Val Ala Phe
420 425 430

Asn Gly Ile Phe Asp Gly Leu Leu Ser Leu Lys Val Leu Lys Met Ala
435 440 445

Gly Asn Ser Phe Gln Glu Asn Phe Leu Pro Asp Ile Phe Thr Asp Leu
450 455 460

Lys Asn Leu Thr Phe Leu Asp Leu Ser Gln Cys Gln Leu Glu Gln Leu
465 470 475 480

Ser Pro Thr Ala Phe Asp Thr Leu Asn Lys Leu Gln Val Leu Asn Met
485 490 495

Ser His Asn Asn Phe Phe Ser Leu Asp Thr Phe Pro Tyr Lys Cys Leu
500 505 510

Pro Ser Leu Gln Val Leu Asp Tyr Ser Leu Asn His Ile Met Thr Ser
515 520 525

Asn Asn Gln Glu Leu Gln His Phe Pro Ser Ser Leu Ala Phe Leu Asn
530 535 540

Leu Thr Gln Asn Asp Phe Ala Cys Thr Cys Glu His Gln Ser Phe Leu
545 550 555 560

Gln Trp Ile Lys Asp Gln Arg Gln Leu Leu Val Glu Ala Glu Arg Met
565 570 575

Glu Cys Ala Thr Pro Ser Asp Lys Gln Gly Met Pro Val Leu Ser Leu
580 585 590

Asn Ile Thr Cys Gln Met Asn Lys Thr Ile Ile Gly Val Ser Val Phe
595 600 605

Ser Val Leu Val Val Ser Val Val Ala Val Leu Val Tyr Lys Phe Tyr
610 615 620

Phe His Leu Met Leu Leu Ala Gly Cys Ile Xaa Tyr Gly Arg Gly Glu
625 630 635 640

Asn Ile Tyr Asp Ala Phe Val Ile Tyr Ser Ser Gln Asp Glu Asp Trp
645 650 655

Val Arg Asn Glu Leu Val Lys Asn Leu Glu Glu Gly Val Pro Pro Phe
660 665 670

Gln Leu Cys Leu His Tyr Arg Asp Phe Ile Pro Gly Val Ala Ile Ala
675 680 685

Ala Asn Ile Ile His Glu Gly Phe His Lys Ser Arg Lys Val Ile Val
690 695 700

Val Val Ser Gln His Phe Ile Gln Ser Arg Trp Cys Ile Phe Glu Tyr
705 710 715 720

Glu Ile Ala Gln Thr Trp Gln Phe Leu Ser Ser Arg Ala Gly Ile Ile
725 730 735

Phe Ile Val Leu Gln Lys Val Glu Lys Thr Leu Leu Arg Gln Gln Val
740 745 750

Glu Leu Tyr Arg Leu Leu Ser Arg Asn Thr Tyr Leu Glu Trp Glu Asp
755 760 765

Ser Val Leu Gly Gln His Ile Phe Trp Arg Arg Leu Arg Lys Ala Leu
770 775 780

Leu Asp Gly Arg Ser Trp Asn Pro Glu Glu Gln
785 790 795

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<211> 2238
<212> DNA
<213> Cebus capucinus

<400> 13

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cacggctctgg ctgggttaga agtccatcgt ttgggtctgg gagaatttag aatgaaaga	540
aatattgaag actttgacaa atctgctctg gaggcctgt gcaatttgac catcaaagaa	600
ttccgattag catacttaga caactttcca gatgatatta ttgacttatt taattgtttg	660
gtaaatgttt cttcatttc cctgttgagt gtgtatatta aaagagtaga agactttct	720
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gatttccagc attccaattt gaaacaaatg agtgagttt cagtatttct atcactcaga	1080
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ttcattgtcc tgcagaaggt ggagaagtcc ctgctcaggc agcaggtgga gctgtaccgc	2100
cttctcagca ggaacaccta cctggagtgg gaggacagtg tcctgggag gcatatcttc	2160
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<213> Cebus capucinus

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ctc tcc acc tta ata ttg aca gga aat cct atc cag aat tta gcc ctg	96
Leu Ser Thr Leu Ile Leu Thr Gly Asn Pro Ile Gln Asn Leu Ala Leu	
20 25 30	
gga gcc ttt tct gga cta tca agt tta cag aaa ctg gta gct gtg gag	144
Gly Ala Phe Ser Gly Leu Ser Ser Leu Gln Lys Leu Val Ala Val Glu	
35 40 45	
aca cat ctg tta tcg cta gaa agc ttc ccc att gga cat ctc aaa act	192
Thr His Leu Leu Ser Leu Glu Ser Phe Pro Ile Gly His Leu Lys Thr	
50 55 60	
ttg aag gac ctt aat gtg gct cac aat cta atc caa tct ttc aaa tta	240
Leu Lys Asp Leu Asn Val Ala His Asn Leu Ile Gln Ser Phe Lys Leu	
65 70 75 80	
cct gag tat ttt tct aat ctg acc aat cta gag cac ttg gac ctt tct	288
Pro Glu Tyr Phe Ser Asn Leu Thr Asn Leu Glu His Leu Asp Leu Ser	
85 90 95	
agt aac aat att caa aat att tat tgc aaa gac ttg cag gtt cta cat	336
Ser Asn Asn Ile Gln Asn Ile Tyr Cys Lys Asp Leu Gln Val Leu His	
100 105 110	
caa atg ccc cta ctc aat ctc tct tta gac ctg tcc ctg aac cct ata	384
Gln Met Pro Leu Leu Asn Leu Ser Leu Asp Leu Ser Leu Asn Pro Ile	
115 120 125	

aac ttt att cag cca ggt gca ttt aaa gaa att agg ctc cgt aag ctg Asn Phe Ile Gln Pro Gly Ala Phe Lys Glu Ile Arg Leu Arg Lys Leu 130 135 140	432
act ttg aga aat aat ttt gat agt tta aat gta atg aaa act tgc att Thr Leu Arg Asn Asn Phe Asp Ser Leu Asn Val Met Lys Thr Cys Ile 145 150 155 160	480
cac ggt ctg gct ggg tta gaa gtc cat cgt ttg gtt ctg gga gaa ttt His Gly Leu Ala Gly Leu Glu Val His Arg Leu Val Leu Gly Glu Phe 165 170 175	528
aga aat gaa aga aat att gaa gac ttt gac aaa tct gct ctg gag ggc Arg Asn Glu Arg Asn Ile Glu Asp Phe Asp Lys Ser Ala Leu Glu Gly 180 185 190	576
ctg tgc aat ttg acc atc aaa gaa ttc cga tta gca tac tta gac aac Leu Cys Asn Leu Thr Ile Lys Glu Phe Arg Leu Ala Tyr Leu Asp Asn 195 200 205	624
ttt cca gat gat att att gac tta ttt aat tgt ttg gta aat gtt tct Phe Pro Asp Asp Ile Ile Asp Leu Phe Asn Cys Leu Val Asn Val Ser 210 215 220	672
tca ttt tcc ctg ttg agt gtg tat att aaa aga gta gaa gac ttt tct Ser Phe Ser Leu Leu Ser Val Tyr Ile Lys Arg Val Glu Asp Phe Ser 225 230 235 240	720
tat aat ttc aga tgg caa cat tta gaa tta gtt aac tgt ata ttt caa Tyr Asn Phe Arg Trp Gln His Leu Glu Leu Val Asn Cys Ile Phe Gln 245 250 255	768
cag ttt cct cca ctg aaa ctc aaa tct ctc aaa agg ctt act ttc agt Gln Phe Pro Pro Leu Lys Leu Lys Ser Leu Lys Arg Leu Thr Phe Ser 260 265 270	816
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gag ttt cta gat ctc agt aga aat ggc ttg agt ttc aaa ggt tgc tgt Glu Phe Leu Asp Leu Ser Arg Asn Gly Leu Ser Phe Lys Gly Cys Cys 290 295 300	912
tct caa tct gat ttt ggg acg acc agc cta aag tat tta gat ctg agc Ser Gln Ser Asp Phe Gly Thr Thr Ser Leu Lys Tyr Leu Asp Leu Ser 305 310 315 320	960
ttc aat gat gtt att acc atg agt tca aac ttc tta ggc tta gaa caa Phe Asn Asp Val Ile Thr Met Ser Ser Asn Phe Leu Gly Leu Glu Gln 325 330 335	1008
cta gaa cac ttg gat ttc cag cat tcc aat ttg aaa caa atg agt gag Leu Glu His Leu Asp Phe Gln His Ser Asn Leu Lys Gln Met Ser Glu 340 345 350	1056
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cat act cac acc aga gtt gct ttc aat ggc atc ttt aat ggc ttg ttc	1152
His Thr His Thr Arg Val Ala Phe Asn Gly Ile Phe Asn Gly Leu Phe	
370 375 380	
agt ctc aaa gtc ttg aaa atg gct gga aat tct ttc cag caa aac ttc	1200
Ser Leu Lys Val Leu Lys Met Ala Gly Asn Ser Phe Gln Gln Asn Phe	
385 390 395 400	
ctt gca gat atc ttc aca gat ctg aat aac ttg ata ttc ctg gac ctt	1248
Leu Ala Asp Ile Phe Thr Asp Leu Asn Asn Leu Ile Phe Leu Asp Leu	
405 410 415	
tct gag tgt caa ctg gag cag ttg tct cca aca gca ttt gac tca ctt	1296
Ser Glu Cys Gln Leu Glu Gln Leu Ser Pro Thr Ala Phe Asp Ser Leu	
420 425 430	
ccc aga ctt cag ata cta aat atg agc cac aac aag ttc ttt gca ttg	1344
Pro Arg Leu Gln Ile Leu Asn Met Ser His Asn Lys Phe Phe Ala Leu	
435 440 445	
gat aca ttt cct tat aag cat ctc tac tcc ctc cac gtt ctg gat tac	1392
Asp Thr Phe Pro Tyr Lys His Leu Tyr Ser Leu His Val Leu Asp Tyr	
450 455 460	
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Ser Leu Asn His Ile Gly Thr Ser Lys Asn Gln Glu Leu Gln His Phe	
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cca agt agt cta gct ttc tta aat ctt actcaa aat gac ttt gct tgt	1488
Pro Ser Ser Leu Ala Phe Leu Asn Leu Thr Gln Asn Asp Phe Ala Cys	
485 490 495	
act tgt gaa cac cag agt ttc ctg cag tgg atc aag gac cag agg cg	1536
Thr Cys Glu His Gln Ser Phe Leu Gln Trp Ile Lys Asp Gln Arg Arg	
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cta ttg gtg gaa gtt gaa cga atg gaa tgc gca aca cct tta aat agg	1584
Leu Leu Val Glu Val Glu Arg Met Glu Cys Ala Thr Pro Leu Asn Arg	
515 520 525	
aag ggc ata cct gtg ctg agt ttg aat atc acc tgt cag atg agt aag	1632
Lys Gly Ile Pro Val Leu Ser Leu Asn Ile Thr Cys Gln Met Ser Lys	
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acc atc att ggt gtg tca gtg ctc agt gtg ctt gtg gta tct gtt gta	1680
Thr Ile Ile Gly Val Ser Val Leu Ser Val Leu Val Val Ser Val Val	
545 550 555 560	
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Ala Val Leu Val Tyr Lys Phe Tyr Phe His Leu Met Leu Leu Ala Gly	
565 570 575	
tgc ata aag tat ggt aga ggt gaa aac acc tat gat gcc ttt gtt atc	1776
Cys Ile Lys Tyr Gly Arg Gly Glu Asn Thr Tyr Asp Ala Phe Val Ile	
580 585 590	
tac tca agc cag gat gag gac tgg gta agg aat gaa cta gta aag aat	1824
Tyr Ser Ser Gln Asp Glu Asp Trp Val Arg Asn Glu Leu Val Lys Asn	
595 600 605	

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ctg agc agt cgt gct ggt atc atc ttc att gtc ctg cag aag gtg gag Leu Ser Ser Arg Ala Gly Ile Ile Phe Ile Val Leu Gln Lys Val Glu 675 680 685	2064
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<212> PRT
<213> Cebus capucinus

<400> 15

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Gly Ala Phe Ser Gly Leu Ser Ser Leu Gln Lys Leu Val Ala Val Glu
35 40 45

Thr His Leu Leu Ser Leu Glu Ser Phe Pro Ile Gly His Leu Lys Thr
50 55 60

Leu Lys Asp Leu Asn Val Ala His Asn Leu Ile Gln Ser Phe Lys Leu
65 70 75 80

Pro Glu Tyr Phe Ser Asn Leu Thr Asn Leu Glu His Leu Asp Leu Ser
85 90 95

Ser Asn Asn Ile Gln Asn Ile Tyr Cys Lys Asp Leu Gln Val Leu His
100 105 110

Gln Met Pro Leu Leu Asn Leu Ser Leu Asp Leu Ser Leu Asn Pro Ile
115 120 125

Asn Phe Ile Gln Pro Gly Ala Phe Lys Glu Ile Arg Leu Arg Lys Leu
130 135 140

Thr Leu Arg Asn Asn Phe Asp Ser Leu Asn Val Met Lys Thr Cys Ile
145 150 155 160

His Gly Leu Ala Gly Leu Glu Val His Arg Leu Val Leu Gly Glu Phe
165 170 175

Arg Asn Glu Arg Asn Ile Glu Asp Phe Asp Lys Ser Ala Leu Glu Gly
180 185 190

Leu Cys Asn Leu Thr Ile Lys Glu Phe Arg Leu Ala Tyr Leu Asp Asn
195 200 205

Phe Pro Asp Asp Ile Ile Asp Leu Phe Asn Cys Leu Val Asn Val Ser
210 215 220

Ser Phe Ser Leu Leu Ser Val Tyr Ile Lys Arg Val Glu Asp Phe Ser
225 230 235 240

Tyr Asn Phe Arg Trp Gln His Leu Glu Leu Val Asn Cys Ile Phe Gln
245 250 255

Gln Phe Pro Pro Leu Lys Leu Lys Ser Leu Lys Arg Leu Thr Phe Ser
260 265 270

Lys Asn Lys Gly Arg Asn His Phe Ala Glu Val Asp Leu Pro Ser Leu
275 280 285

Glu Phe Leu Asp Leu Ser Arg Asn Gly Leu Ser Phe Lys Gly Cys Cys
290 295 300

Ser Gln Ser Asp Phe Gly Thr Thr Ser Leu Lys Tyr Leu Asp Leu Ser
305 310 315 320

Phe Asn Asp Val Ile Thr Met Ser Ser Asn Phe Leu Gly Leu Glu Gln
325 330 335

Leu Glu His Leu Asp Phe Gln His Ser Asn Leu Lys Gln Met Ser Glu
340 345 350

Phe Ser Val Phe Leu Ser Leu Arg Asn Leu Ile Tyr Leu Asp Ile Ser
355 360 365

His Thr His Thr Arg Val Ala Phe Asn Gly Ile Phe Asn Gly Leu Phe
370 375 380

Ser Leu Lys Val Leu Lys Met Ala Gly Asn Ser Phe Gln Gln Asn Phe
385 390 395 400

Leu Ala Asp Ile Phe Thr Asp Leu Asn Asn Leu Ile Phe Leu Asp Leu
405 410 415

Ser Glu Cys Gln Leu Glu Gln Leu Ser Pro Thr Ala Phe Asp Ser Leu
420 425 430

Pro Arg Leu Gln Ile Leu Asn Met Ser His Asn Lys Phe Phe Ala Leu
435 440 445

Asp Thr Phe Pro Tyr Lys His Leu Tyr Ser Leu His Val Leu Asp Tyr
450 455 460

Ser Leu Asn His Ile Gly Thr Ser Lys Asn Gln Glu Leu Gln His Phe
465 470 475 480

Pro Ser Ser Leu Ala Phe Leu Asn Leu Thr Gln Asn Asp Phe Ala Cys
485 490 495

Thr Cys Glu His Gln Ser Phe Leu Gln Trp Ile Lys Asp Gln Arg Arg
500 505 510

Leu Leu Val Glu Val Glu Arg Met Glu Cys Ala Thr Pro Leu Asn Arg
515 520 525

Lys Gly Ile Pro Val Leu Ser Leu Asn Ile Thr Cys Gln Met Ser Lys
530 535 540

Thr Ile Ile Gly Val Ser Val Leu Ser Val Leu Val Val Ser Val Val
545 550 555 560

Ala Val Leu Val Tyr Lys Phe Tyr Phe His Leu Met Leu Leu Ala Gly
565 570 575

Cys Ile Lys Tyr Gly Arg Gly Glu Asn Thr Tyr Asp Ala Phe Val Ile
580 585 590

Tyr Ser Ser Gln Asp Glu Asp Trp Val Arg Asn Glu Leu Val Lys Asn
595 600 605

Leu Glu Glu Gly Val Pro Pro Phe Gln Leu Cys Leu His Tyr Arg Asp
610 615 620

Phe Ile Pro Gly Val Ala Ile Ala Ala Asn Ile Ile His Glu Gly Phe
625 630 635 640

His Lys Ser Arg Lys Val Ile Val Val Val Ser Gln His Phe Ile Gln
645 650 655

Ser Arg Trp Cys Ile Phe Glu Tyr Glu Ile Ala Gln Thr Trp Gln Phe
660 665 670

Leu Ser Ser Arg Ala Gly Ile Ile Phe Ile Val Leu Gln Lys Val Glu
675 680 685

Lys Ser Leu Leu Arg Gln Gln Val Glu Leu Tyr Arg Leu Leu Ser Arg
690 695 700

Asn Thr Tyr Leu Glu Trp Glu Asp Ser Val Leu Gly Arg His Ile Phe
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Trp Arg Arg Leu Arg Lys Ala Leu Leu Asn Gly Arg Pro Trp Ser Pro
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Glu Gly Thr Val Gly Ala Gly Cys Asp
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<213> Saimiri sciureus

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atc ccc gac aac atc ccc ttc tca act aag aac ctg gac ctg agc ttt	96
Ile Pro Asp Asn Ile Pro Phe Ser Thr Lys Asn Leu Asp Leu Ser Phe	
20 25 30	
aac ccc ctg agg cat tta ggc agc cat agc ttc ttc aat ttc cca gaa	144
Asn Pro Leu Arg His Leu Gly Ser His Ser Phe Phe Asn Phe Pro Glu	
35 40 45	
ctg cag gtg ctg gat tta tcc agg tgt gac atc cag aca atc gaa gat	192
Leu Gln Val Leu Asp Leu Ser Arg Cys Asp Ile Gln Thr Ile Glu Asp	
50 55 60	
ggg gca tat cag agc cta agc cac ctc tcc acc tta ata ttg aca gga	240
Gly Ala Tyr Gln Ser Leu Ser His Leu Ser Thr Leu Ile Leu Thr Gly	
65 70 75 80	
aat cct atc cag aat tta gcc ctg gga gcc ttt tct gga cta tca agt	288
Asn Pro Ile Gln Asn Leu Ala Leu Gly Ala Phe Ser Gly Leu Ser Ser	
85 90 95	
tta cag aag ctg gtg gct gtg gag aca cat ctg tta tca cta gag aac	336
Leu Gln Lys Leu Val Ala Val Glu Thr His Leu Leu Ser Leu Glu Asn	

100

105

110

ttc ccc att gga cat ctc aaa act ttg aag gac ctt aat gtg gct cac Phe Pro Ile Gly His Leu Lys Thr Leu Lys Asp Leu Asn Val Ala His 115 120 125	384
aat cta atc caa tct ttc aaa tta cct gag tat ttt tct aat ctg acc Asn Leu Ile Gln Ser Phe Lys Leu Pro Glu Tyr Phe Ser Asn Leu Thr 130 135 140	432
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tgc aaa gac ttg cag gtt cta cat caa atg ccc cta ctc aat ctc tct Cys Lys Asp Leu Gln Val Leu His Gln Met Pro Leu Leu Asn Leu Ser 165 170 175	528
tta gac ctg tcc ctg aac cct ata aac ttt att caa cca ggt gcg ttt Leu Asp Leu Ser Leu Asn Pro Ile Asn Phe Ile Gln Pro Gly Ala Phe 180 185 190	576
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cat cgt ttg gtt ctg gga gaa ttt aga aat gaa aga aat att gaa gac His Arg Leu Val Leu Gly Glu Phe Arg Asn Glu Arg Asn Ile Glu Asp 225 230 235 240	720
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ttc cga tta gct tac tta gat gac ttt cta gat gat att att gac tta Phe Arg Leu Ala Tyr Leu Asp Asp Phe Leu Asp Asp Ile Ile Asp Leu 260 265 270	816
ttt aac tgt tta gca aat gtt tct tca ttt tcc ctg gtg aat gtg cat Phe Asn Cys Leu Ala Asn Val Ser Ser Phe Ser Leu Val Asn Val His 275 280 285	864
att aaa aga gta gaa gac ttt tct tat aat ttt aga tgg caa cat tta Ile Lys Arg Val Glu Asp Phe Ser Tyr Asn Phe Arg Trp Gln His Leu 290 295 300	912
gaa tta gtt aac tgt gta ttt caa cag ttt cct cca ctg aaa ctc aaa Glu Leu Val Asn Cys Val Phe Gln Gln Phe Pro Pro Leu Lys Leu Lys 305 310 315 320	960
tct ctc aaa agg ctt act ttc act gcc aac aaa ggt agg aat cat ttt Ser Leu Lys Arg Leu Thr Phe Thr Ala Asn Lys Gly Arg Asn His Phe 325 330 335	1008
tca gaa gtt gat ctt cca agc ctt gag ttt cta gat ctc agt aga aat Ser Glu Val Asp Leu Pro Ser Leu Glu Phe Leu Asp Leu Ser Arg Asn	1056

340

345

350

ggc ttg agt ttc aaa ggt tgc tgt tct caa tct gat ttt ggg acg acc Gly Leu Ser Phe Lys Gly Cys Cys Ser Gln Ser Asp Phe Gly Thr Thr 355 360 365	1104
agc cta aag tat tta gat ctg agc ttc aat gac gtt att acc atg ggt Ser Leu Lys Tyr Leu Asp Leu Ser Phe Asn Asp Val Ile Thr Met Gly 370 375 380	1152
tca aac ttc tta ggc tta gaa caa cta gaa cac ttg gat ttc cag cat Ser Asn Phe Leu Gly Leu Glu Gln Leu Glu His Leu Asp Phe Gln His 385 390 395 400	1200
tcc aat ttg aaa caa atg agt gag ttt tca gta ttc cta tca ctc aga Ser Asn Leu Lys Gln Met Ser Glu Phe Ser Val Phe Leu Ser Leu Arg 405 410 415	1248
aac ctc att tac ctt gac att tct cat act cac acc aga gtt gct ttc Asn Leu Ile Tyr Leu Asp Ile Ser His Thr His Thr Arg Val Ala Phe 420 425 430	1296
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gga aat tct ttc cag caa aac ttc ctt gaa gat atc ttc acr gat ctg Gly Asn Ser Phe Gln Gln Asn Phe Leu Glu Asp Ile Phe Xaa Asp Leu 450 455 460	1392
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agc cac aac aac ttc ttt gca ttg gat aca ttc cct tac aag cat ctc Ser His Asn Asn Phe Phe Ala Leu Asp Thr Phe Pro Tyr Lys His Leu 500 505 510	1536
tac tcc ctc cag gtt ctg gat tac agt ctc aat cat ata ggg act tcc Tyr Ser Leu Gln Val Leu Asp Tyr Ser Leu Asn His Ile Gly Thr Ser 515 520 525	1584
aaa aat cag gaa ctg cag cat ttt cca agt agt cta gct ttc tta aat Lys Asn Gln Glu Leu Gln His Phe Pro Ser Ser Leu Ala Phe Leu Asn 530 535 540	1632
ctt act caa aat gac ttt gct tgt act tgt gaa cac cag agt ttc ctg Leu Thr Gln Asn Asp Phe Ala Cys Thr Cys Glu His Gln Ser Phe Leu 545 550 555 560	1680
cag tgg atc aag gac cag agg cgg ctg ttg gtg gaa gtt gaa caa atg Gln Trp Ile Lys Asp Gln Arg Arg Leu Leu Val Glu Val Glu Gln Met 565 570 575	1728
gaa tgt gca aca cct tta aat agg aag ggc ata cct gtg ctg agt ttg Glu Cys Ala Thr Pro Leu Asn Arg Lys Gly Ile Pro Val Leu Ser Leu	1776

580	585	590	
aat atc acc tgt cag atg agt aag act atc att ggt gtg tca gtg ctc Asn Ile Thr Cys Gln Met Ser Lys Thr Ile Ile Gly Val Ser Val Leu 595 600 605			1824
agt gtg ctt gtg gta tct gtt gta gca gtt ctg gtc tat aag ttc tat Ser Val Leu Val Val Ser Val Val Ala Val Leu Val Tyr Lys Phe Tyr 610 615 620			1872
ttt cac ctg atg ctt ctt gct ggc tgc ata aag tat ggt aga ggt gaa Phe His Leu Met Leu Leu Ala Gly Cys Ile Lys Tyr Gly Arg Gly Glu 625 630 635 640			1920
aac acc tat gat gcc ttt gtt atc tac tca agc cag gat gag gac tgg Asn Thr Tyr Asp Ala Phe Val Ile Tyr Ser Ser Gln Asp Glu Asp Trp 645 650 655			1968
gta agg aat gaa cta gta aag aat tta gaa gaa ggg gtg cct ccc ttt Val Arg Asn Glu Leu Val Lys Asn Leu Glu Glu Gly Val Pro Pro Phe 660 665 670			2016
cag ctc tgc ctt cac tac aga gac ttt att ccc ggt gtg gcc att gct Gln Leu Cys Leu His Tyr Arg Asp Phe Ile Pro Gly Val Ala Ile Ala 675 680 685			2064
gcc aac atc atc cat gaa ggt ttc cat aaa agc cga aag gtg att gtt Ala Asn Ile Ile His Glu Gly Phe His Lys Ser Arg Lys Val Ile Val 690 695 700			2112
gtg gta tct cag cac ttc atc cag agc cgc tgg tgt atc ttt gaa tat Val Val Ser Gln His Phe Ile Gln Ser Arg Trp Cys Ile Phe Glu Tyr 705 710 715 720			2160
gag att gct cag acc tgg cag ttt ctg agc agt cgt gct ggt atc atc Glu Ile Ala Gln Thr Trp Gln Phe Leu Ser Ser Arg Ala Gly Ile Ile 725 730 735			2208
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agt gtc ctg ggg agg cac atc ttc tgg aga cga ctc aga aaa gcc ctg Ser Val Leu Gly Arg His Ile Phe Trp Arg Arg Leu Arg Lys Ala Leu 770 775 780			2352
ctg gat ggt aga ccg tgg aat cca gaa gga aca gtg ggt gca gga tgc Leu Asp Gly Arg Pro Trp Asn Pro Glu Gly Thr Val Gly Ala Gly Cys 785 790 795 800			2400
gaa tag Glu			2406

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<212> PRT
<213> Saimiri sciureus

<220>
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<222> (14)..(14)
<223> The 'Xaa' at location 14 stands for Leu, or Phe.

<220>
<221> misc_feature
<222> (462)..(462)
<223> The 'Xaa' at location 462 stands for Thr.

<400> 18

Val Val Pro Asn Val Thr Tyr Gln Cys Met Glu Leu Asn Xaa Tyr Lys
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Ile Pro Asp Asn Ile Pro Phe Ser Thr Lys Asn Leu Asp Leu Ser Phe
20 25 30

Asn Pro Leu Arg His Leu Gly Ser His Ser Phe Phe Asn Phe Pro Glu
35 40 45

Leu Gln Val Leu Asp Leu Ser Arg Cys Asp Ile Gln Thr Ile Glu Asp
50 55 60

Gly Ala Tyr Gln Ser Leu Ser His Leu Ser Thr Leu Ile Leu Thr Gly
65 70 75 80

Asn Pro Ile Gln Asn Leu Ala Leu Gly Ala Phe Ser Gly Leu Ser Ser
85 90 95

Leu Gln Lys Leu Val Ala Val Glu Thr His Leu Leu Ser Leu Glu Asn
100 105 110

Phe Pro Ile Gly His Leu Lys Thr Leu Lys Asp Leu Asn Val Ala His
115 120 125

Asn Leu Ile Gln Ser Phe Lys Leu Pro Glu Tyr Phe Ser Asn Leu Thr
130 135 140

Asn Leu Glu His Leu Asp Leu Ser Ser Asn Asn Ile Gln Asn Ile Tyr
145 150 155 160

Cys Lys Asp Leu Gln Val Leu His Gln Met Pro Leu Leu Asn Leu Ser
165 170 175

Leu Asp Leu Ser Leu Asn Pro Ile Asn Phe Ile Gln Pro Gly Ala Phe
180 185 190

Lys Glu Ile Arg Leu His Lys Leu Thr Leu Arg Asn Asn Phe Asp Ser
195 200 205

Leu Asn Ala Met Lys Thr Cys Ile Gln Gly Leu Ala Gly Leu Glu Val
210 215 220

His Arg Leu Val Leu Gly Glu Phe Arg Asn Glu Arg Asn Ile Glu Asp
225 230 235 240

Phe Asp Lys Ser Ala Leu Glu Gly Leu Cys Asn Leu Thr Ile Asn Glu
245 250 255

Phe Arg Leu Ala Tyr Leu Asp Asp Phe Leu Asp Asp Ile Ile Asp Leu
260 265 270

Phe Asn Cys Leu Ala Asn Val Ser Ser Phe Ser Leu Val Asn Val His
275 280 285

Ile Lys Arg Val Glu Asp Phe Ser Tyr Asn Phe Arg Trp Gln His Leu
290 295 300

Glu Leu Val Asn Cys Val Phe Gln Gln Phe Pro Pro Leu Lys Leu Lys
305 310 315 320

Ser Leu Lys Arg Leu Thr Phe Thr Ala Asn Lys Gly Arg Asn His Phe
325 330 335

Ser Glu Val Asp Leu Pro Ser Leu Glu Phe Leu Asp Leu Ser Arg Asn
340 345 350

Gly Leu Ser Phe Lys Gly Cys Cys Ser Gln Ser Asp Phe Gly Thr Thr
355 360 365

Ser Leu Lys Tyr Leu Asp Leu Ser Phe Asn Asp Val Ile Thr Met Gly
370 375 380

Ser Asn Phe Leu Gly Leu Glu Gln Leu Glu His Leu Asp Phe Gln His
385 390 395 400

Ser Asn Leu Lys Gln Met Ser Glu Phe Ser Val Phe Leu Ser Leu Arg
405 410 415

Asn Leu Ile Tyr Leu Asp Ile Ser His Thr His Thr Arg Val Ala Phe
420 425 430

Asn Gly Ile Phe Asn Gly Leu Phe Ser Leu Lys Val Leu Lys Met Ala
435 440 445

Gly Asn Ser Phe Gln Gln Asn Phe Leu Glu Asp Ile Phe Xaa Asp Leu
450 455 460

Asn Asn Leu Ile Phe Leu Asp Leu Ser Glu Cys Gln Leu Glu Gln Leu
465 470 475 480

Ser Pro Thr Ala Phe Asp Ser Leu Pro Arg Leu Arg Ile Leu Asn Met
485 490 495

Ser His Asn Asn Phe Phe Ala Leu Asp Thr Phe Pro Tyr Lys His Leu
500 505 510

Tyr Ser Leu Gln Val Leu Asp Tyr Ser Leu Asn His Ile Gly Thr Ser
515 520 525

Lys Asn Gln Glu Leu Gln His Phe Pro Ser Ser Leu Ala Phe Leu Asn
530 535 540

Leu Thr Gln Asn Asp Phe Ala Cys Thr Cys Glu His Gln Ser Phe Leu
545 550 555 560

Gln Trp Ile Lys Asp Gln Arg Arg Leu Leu Val Glu Val Glu Gln Met
565 570 575

Glu Cys Ala Thr Pro Leu Asn Arg Lys Gly Ile Pro Val Leu Ser Leu
580 585 590

Asn Ile Thr Cys Gln Met Ser Lys Thr Ile Ile Gly Val Ser Val Leu
595 600 605

Ser Val Leu Val Val Ser Val Val Ala Val Leu Val Tyr Lys Phe Tyr
610 615 620

Phe His Leu Met Leu Leu Ala Gly Cys Ile Lys Tyr Gly Arg Gly Glu
625 630 635 640

Asn Thr Tyr Asp Ala Phe Val Ile Tyr Ser Ser Gln Asp Glu Asp Trp
645 650 655

Val Arg Asn Glu Leu Val Lys Asn Leu Glu Glu Gly Val Pro Pro Phe
660 665 670

Gln Leu Cys Leu His Tyr Arg Asp Phe Ile Pro Gly Val Ala Ile Ala
675 680 685

Ala Asn Ile Ile His Glu Gly Phe His Lys Ser Arg Lys Val Ile Val
690 695 700

Val Val Ser Gln His Phe Ile Gln Ser Arg Trp Cys Ile Phe Glu Tyr
705 710 715 720

Glu Ile Ala Gln Thr Trp Gln Phe Leu Ser Ser Arg Ala Gly Ile Ile
725 730 735

Phe Ile Val Leu Gln Lys Val Glu Lys Ser Leu Leu Arg Gln Gln Val
740 745 750

Glu Leu Tyr Arg Leu Leu Ser Arg Asn Thr Tyr Leu Glu Trp Glu Asp
755 760 765

Ser Val Leu Gly Arg His Ile Phe Trp Arg Arg Leu Arg Lys Ala Leu
770 775 780

Leu Asp Gly Arg Pro Trp Asn Pro Glu Gly Thr Val Gly Ala Gly Cys
785 790 795 800

Glu

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tatagcttcc tccgtttcc agaactgcag gtgctggatt tatccaggtg tgaaatccag	180
acaattgaag atggggcata tcagagccta agccacctct ccacctaattt attgacagga	240
aaccccatcc agagtttagc cctgggagcc tttctggac tatcaagttt acagaagctg	300
gtggctgtgg agacaaatct agcatctcta gagaacttcc ccattggaca tctcaaaaact	360
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tcattttccc tggtagtgtt gaatattaaa aggtagaag acttttctta taatttcaga	900
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cagtggatca aggaccagag gcagctctt gttggaaagctg aacgaatgga atgtgcaaca	1740
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aacatctatg atgcctttgt tatctactca agccaggatg aggactgggt aaggaatgag	1980
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aaggtgattt ttgtgggtgc ccagcacttc atccagagcc gctgggtat cttgaatat	2160
gagattgctc agacctggca gtttctgagc agtcgtgcag gcataatctt cattgtcctg	2220

cagaagggtgg agaagaccct gctcaggcag caggtggagc tgtaccgcct tctcagcagg 2280
 aacacttacc tggagtggga ggacagtgtc ctagggcagc acatcttctg gagacgactc 2340
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atc ccc gac aac atc ccc ttc tca acc aag aac ctg gac ctg agc ttt 96
 Ile Pro Asp Asn Ile Pro Phe Ser Thr Lys Asn Leu Asp Leu Ser Phe
 20 25 30

aat ccc ctg agg cat tta ggc agc tat agc ttc ctc cgt ttt cca gaa 144
 Asn Pro Leu Arg His Leu Gly Ser Tyr Ser Phe Leu Arg Phe Pro Glu
 35 40 45

ctg cag gtg ctg gat tta tcc agg tgt gaa atc cag aca att gaa gat 192
 Leu Gln Val Leu Asp Leu Ser Arg Cys Glu Ile Gln Thr Ile Glu Asp
 50 55 60

ggg gca tat cag agc cta agc cac ctc tcc acc tta ata ttg aca gga 240
 Gly Ala Tyr Gln Ser Leu Ser His Leu Ser Thr Leu Ile Leu Thr Gly
 65 70 75 80

aac ccc atc cag agt tta gcc ctg gga gcc ttt tct gga cta tca agt 288
 Asn Pro Ile Gln Ser Leu Ala Leu Gly Ala Phe Ser Gly Leu Ser Ser
 85 90 95

tta cag aag ctg gtg gct gtg gag aca aat cta gca tct cta gag aac 336
 Leu Gln Lys Leu Val Ala Val Glu Thr Asn Leu Ala Ser Leu Glu Asn
 100 105 110

ttc ccc att gga cat ctc aaa act ttg aaa gaa ctt aat gtg gct cac 384
 Phe Pro Ile Gly His Leu Lys Thr Leu Lys Glu Leu Asn Val Ala His
 115 120 125

aat ctt atc cag tct ttc aaa tta cct gag tat ttt tct aat ctg acc 432
 Asn Leu Ile Gln Ser Phe Lys Leu Pro Glu Tyr Phe Ser Asn Leu Thr
 130 135 140

aat cta gag cac ttg gac ctt tcc agt aac aag att caa aat att tat 480
 Asn Leu Glu His Leu Asp Leu Ser Ser Asn Lys Ile Gln Asn Ile Tyr
 145 150 155 160

tgc aaa gac ttg cag gtt cta cat caa atg ccc cta ccc aat ctc tct 528
 Cys Lys Asp Leu Gln Val Leu His Gln Met Pro Leu Pro Asn Leu Ser

165

170

175

tta gac ctg tcc ctg aac cct ata aac ttt atc caa cca ggt gca ttt Leu Asp Leu Ser Leu Asn Pro Ile Asn Phe Ile Gln Pro Gly Ala Phe 180 185 190	576
aaa gaa att agg ctt cat aag ctg act ttg aga agt aat ttt gat gat Lys Glu Ile Arg Leu His Lys Leu Thr Leu Arg Ser Asn Phe Asp Asp 195 200 205	624
tta aat gta atg aaa act tgt att caa ggt ctg gct ggt tta gaa gtc Leu Asn Val Met Lys Thr Cys Ile Gln Gly Leu Ala Gly Leu Glu Val 210 215 220	672
cat cgt ttg gtt ctg gga gaa ttt aga aat gaa aga aac ttg gaa gag His Arg Leu Val Leu Gly Glu Phe Arg Asn Glu Arg Asn Leu Glu Glu 225 230 235 240	720
ttt gac aaa tct gct ctg gag gga ttg tgc aat ttg acc att gaa gaa Phe Asp Lys Ser Ala Leu Glu Gly Leu Cys Asn Leu Thr Ile Glu Glu 245 250 255	768
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att aaa agg gta gaa gac ttt tct tat aat ttc aga tgg caa cat tta Ile Lys Arg Val Glu Asp Phe Ser Tyr Asn Phe Arg Trp Gln His Leu 290 295 300	912
gaa tta gtt aac tgt aaa ttt gaa cag ttt ccc aca ttg gaa ctc gaa Glu Leu Val Asn Cys Lys Phe Glu Gln Phe Pro Thr Leu Glu Leu Glu 305 310 315 320	960
tct ctc aaa agg ctt act ttc act gcc aac aaa ggt ggg aat gcc ttt Ser Leu Lys Arg Leu Thr Phe Thr Ala Asn Lys Gly Gly Asn Ala Phe 325 330 335	1008
tca gaa gtt gat cta cca agc ctt gag ttt cta gat ctc agt aga aat Ser Glu Val Asp Leu Pro Ser Leu Glu Phe Leu Asp Leu Ser Arg Asn 340 345 350	1056
ggc ttg agt ttc aaa ggt tgc tgt tct caa agt gat ttt ggg aca acc Gly Leu Ser Phe Lys Gly Cys Cys Ser Gln Ser Asp Phe Gly Thr Thr 355 360 365	1104
agc cta aag tat tta gat ctg agc ttc aat gat gtt att acc atg ggt Ser Leu Lys Tyr Leu Asp Leu Ser Phe Asn Asp Val Ile Thr Met Gly 370 375 380	1152
tca aac ttc ttg ggc tta gaa caa cta gaa cat ctg gat ttc cag cat Ser Asn Phe Leu Gly Leu Glu Gln Leu Glu His Leu Asp Phe Gln His 385 390 395 400	1200
tcc aat ttg aaa cag atg agt caa ttt tca gta ttc cta tca ctc aga Ser Asn Leu Lys Gln Met Ser Gln Phe Ser Val Phe Leu Ser Leu Arg	1248

405

410

415

aac ctc att tac ctt gac att tct cat act cac acc aca gtt gct ttc Asn Leu Ile Tyr Leu Asp Ile Ser His Thr His Thr Val Ala Phe 420	425	430	1296	
aat ggc att ttc gat ggc ttg ctc agt ctc aaa gtc tta aaa atg gct Asn Gly Ile Phe Asp Gly Leu Leu Ser Leu Lys Val Leu Lys Met Ala 435	440	445	1344	
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tct cca aca gca ttt gac aca ctc aac aag ctt cag gta cta aat atg Ser Pro Thr Ala Phe Asp Thr Leu Asn Lys Leu Gln Val Leu Asn Met 485	490	495	1488	
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ccc tcc ctc cag gtt ctc gat tac agt ctc aat cac ata atg act tcc Pro Ser Leu Gln Val Leu Asp Tyr Ser Leu Asn His Ile Met Thr Ser 515	520	525	1584	
aaa aac cag gaa cct cag cat ttt cca agt agt cta gct ttc tta aat Lys Asn Gln Glu Pro Gln His Phe Pro Ser Ser Leu Ala Phe Leu Asn 530	535	540	1632	
ctt act cag aat gac ttt gct tgt act tgt gaa cac cag agt ttc ctg Leu Thr Gln Asn Asp Phe Ala Cys Thr Cys Glu His Gln Ser Phe Leu 545	550	555	560	1680
cag tgg atc aag gac cag agg cag ctc ttg gtg gaa gct gaa cga atg Gln Trp Ile Lys Asp Gln Arg Gln Leu Leu Val Glu Ala Glu Arg Met 565	570	575	1728	
gaa tgt gca aca cct tca gat aaa cag ggc atg cct gtg ctg agt gtg Glu Cys Ala Thr Pro Ser Asp Lys Gln Gly Met Pro Val Leu Ser Val 580	585	590	1776	
aat att acc tgt cag atg aat aag acc atc att ggt gtt tct gtg ttc Asn Ile Thr Cys Gln Met Asn Lys Thr Ile Ile Gly Val Ser Val Phe 595	600	605	1824	
agt gtg ctt gtg gta tct gtt gta gca gtt ctg gtc tat aag ttc tat Ser Val Leu Val Val Ser Val Val Ala Val Leu Val Tyr Lys Phe Tyr 610	615	620	1872	
ttt cac ctg atg ctt ctt gct ggc tgc ata aag tat ggt aga ggt gaa Phe His Leu Met Leu Leu Ala Gly Cys Ile Lys Tyr Gly Arg Gly Glu 625	630	635	640	1920
ccc atc tat gat gcc ttt gtt atc tac tca agc cag gat gag gac tgg Asn Ile Tyr Asp Ala Phe Val Ile Tyr Ser Ser Gln Asp Glu Asp Trp				1968

645

650

655

gta agg aat gag cta gta aag aat tta gaa gaa ggg gtg cct ccc ttt 2016
 Val Arg Asn Glu Leu Val Lys Asn Leu Glu Glu Gly Val Pro Pro Phe
 660 665 670

cag ctc tgc ctt cac tac aga gac ttt att ccc ggt gtg gcc att gct 2064
 Gln Leu Cys Leu His Tyr Arg Asp Phe Ile Pro Gly Val Ala Ile Ala
 675 680 685

gca aac atc atc cat gaa ggt ttc cat aaa agc cga aag gtg att gtt 2112
 Ala Asn Ile Ile His Glu Gly Phe His Lys Ser Arg Lys Val Ile Val
 690 695 700

gtg gtg tcc cag cac ttc atc cag agc cgc tgg tgt atc ttt gaa tat 2160
 Val Val Ser Gln His Phe Ile Gln Ser Arg Trp Cys Ile Phe Glu Tyr
 705 710 715 720

gag att gct cag acc tgg cag ttt ctg agc agt cgt gca ggc ata atc 2208
 Glu Ile Ala Gln Thr Trp Gln Phe Leu Ser Ser Arg Ala Gly Ile Ile
 725 730 735

ttc att gtc ctg cag aag gtg gag aag acc ctg ctc agg cag cag gtg 2256
 Phe Ile Val Leu Gln Lys Val Glu Lys Thr Leu Leu Arg Gln Gln Val
 740 745 750

gag ctg tac cgc ctt ctc agc agg aac act tac ctg gag tgg gag gac 2304
 Glu Leu Tyr Arg Leu Leu Ser Arg Asn Thr Tyr Leu Glu Trp Glu Asp
 755 760 765

agt gtc cta ggg cag cac atc ttc tgg aga cga ctc aga aaa gcc ctg 2352
 Ser Val Leu Gly Gln His Ile Phe Trp Arg Arg Leu Arg Lys Ala Leu
 770 775 780

ttg gat ggc aga tcg tgg aat cca gaa gaa cag tag 2388
 Leu Asp Gly Arg Ser Trp Asn Pro Glu Glu Gln
 785 790 795

<210> 21

<211> 795

<212> PRT

<213> Papio hamadryas

<400> 21

Val Val Pro Asn Ile Thr Tyr Gln Cys Met Glu Leu Asn Phe Tyr Lys
 1 5 10 15

Ile Pro Asp Asn Ile Pro Phe Ser Thr Lys Asn Leu Asp Leu Ser Phe
 20 25 30

Asn Pro Leu Arg His Leu Gly Ser Tyr Ser Phe Leu Arg Phe Pro Glu
 35 40 45

Leu Gln Val Leu Asp Leu Ser Arg Cys Glu Ile Gln Thr Ile Glu Asp
 50 55 60

Gly Ala Tyr Gln Ser Leu Ser His Leu Ser Thr Leu Ile Leu Thr Gly
65 70 75 80

Asn Pro Ile Gln Ser Leu Ala Leu Gly Ala Phe Ser Gly Leu Ser Ser
85 90 95

Leu Gln Lys Leu Val Ala Val Glu Thr Asn Leu Ala Ser Leu Glu Asn
100 105 110

Phe Pro Ile Gly His Leu Lys Thr Leu Lys Glu Leu Asn Val Ala His
115 120 125

Asn Leu Ile Gln Ser Phe Lys Leu Pro Glu Tyr Phe Ser Asn Leu Thr
130 135 140

Asn Leu Glu His Leu Asp Leu Ser Ser Asn Lys Ile Gln Asn Ile Tyr
145 150 155 160

Cys Lys Asp Leu Gln Val Leu His Gln Met Pro Leu Pro Asn Leu Ser
165 170 175

Leu Asp Leu Ser Leu Asn Pro Ile Asn Phe Ile Gln Pro Gly Ala Phe
180 185 190

Lys Glu Ile Arg Leu His Lys Leu Thr Leu Arg Ser Asn Phe Asp Asp
195 200 205

Leu Asn Val Met Lys Thr Cys Ile Gln Gly Leu Ala Gly Leu Glu Val
210 215 220

His Arg Leu Val Leu Gly Glu Phe Arg Asn Glu Arg Asn Leu Glu Glu
225 230 235 240

Phe Asp Lys Ser Ala Leu Glu Gly Leu Cys Asn Leu Thr Ile Glu Glu
.245 250 255

Phe Arg Leu Thr Tyr Leu Asp Tyr Tyr Leu Asp Asn Ile Ile Asp Leu
260 265 270

Phe Asn Cys Leu Ala Asn Ala Ser Ser Phe Ser Leu Val Ser Val Asn
275 280 285

Ile Lys Arg Val Glu Asp Phe Ser Tyr Asn Phe Arg Trp Gln His Leu
290 295 300

Glu Leu Val Asn Cys Lys Phe Glu Gln Phe Pro Thr Leu Glu Leu Glu
305 310 315 320

Ser Leu Lys Arg Leu Thr Phe Thr Ala Asn Lys Gly Gly Asn Ala Phe
325 330 335

Ser Glu Val Asp Leu Pro Ser Leu Glu Phe Leu Asp Leu Ser Arg Asn
340 345 350

Gly Leu Ser Phe Lys Gly Cys Cys Ser Gln Ser Asp Phe Gly Thr Thr
355 360 365

Ser Leu Lys Tyr Leu Asp Leu Ser Phe Asn Asp Val Ile Thr Met Gly
370 375 380

Ser Asn Phe Leu Gly Leu Glu Gln Leu Glu His Leu Asp Phe Gln His
385 390 395 400

Ser Asn Leu Lys Gln Met Ser Gln Phe Ser Val Phe Leu Ser Leu Arg
405 410 415

Asn Leu Ile Tyr Leu Asp Ile Ser His Thr His Thr Thr Val Ala Phe
420 425 430

Asn Gly Ile Phe Asp Gly Leu Leu Ser Leu Lys Val Leu Lys Met Ala
435 440 445

Gly Asn Ser Phe Gln Glu Asn Phe Leu Pro Asp Ile Phe Thr Asp Leu
450 455 460

Lys Asn Leu Thr Phe Leu Asp Leu Ser Gln Cys Gln Leu Glu Gln Leu
465 470 475 480

Ser Pro Thr Ala Phe Asp Thr Leu Asn Lys Leu Gln Val Leu Asn Met
485 490 495

Ser His Asn Asn Phe Phe Ser Leu Asp Val Phe Pro Tyr Lys Cys Leu
500 505 510

Pro Ser Leu Gln Val Leu Asp Tyr Ser Leu Asn His Ile Met Thr Ser
515 520 525

Lys Asn Gln Glu Pro Gln His Phe Pro Ser Ser Leu Ala Phe Leu Asn
530 535 540

Leu Thr Gln Asn Asp Phe Ala Cys Thr Cys Glu His Gln Ser Phe Leu
545 550 555 560

Gln Trp Ile Lys Asp Gln Arg Gln Leu Leu Val Glu Ala Glu Arg Met
565 570 575

Glu Cys Ala Thr Pro Ser Asp Lys Gln Gly Met Pro Val Leu Ser Val
580 585 590

Asn Ile Thr Cys Gln Met Asn Lys Thr Ile Ile Gly Val Ser Val Phe
595 600 605

Ser Val Leu Val Val Ser Val Val Ala Val Leu Val Tyr Lys Phe Tyr
610 615 620

Phe His Leu Met Leu Leu Ala Gly Cys Ile Lys Tyr Gly Arg Gly Glu
625 630 635 640

Asn Ile Tyr Asp Ala Phe Val Ile Tyr Ser Ser Gln Asp Glu Asp Trp
645 650 655

Val Arg Asn Glu Leu Val Lys Asn Leu Glu Glu Gly Val Pro Pro Phe
660 665 670

Gln Leu Cys Leu His Tyr Arg Asp Phe Ile Pro Gly Val Ala Ile Ala
675 680 685

Ala Asn Ile Ile His Glu Gly Phe His Lys Ser Arg Lys Val Ile Val
690 695 700

Val Val Ser Gln His Phe Ile Gln Ser Arg Trp Cys Ile Phe Glu Tyr
705 710 715 720

Glu Ile Ala Gln Thr Trp Gln Phe Leu Ser Ser Arg Ala Gly Ile Ile
725 730 735

Phe Ile Val Leu Gln Lys Val Glu Lys Thr Leu Leu Arg Gln Gln Val
740 745 750

Glu Leu Tyr Arg Leu Leu Ser Arg Asn Thr Tyr Leu Glu Trp Glu Asp
755 760 765

Ser Val Leu Gly Gln His Ile Phe Trp Arg Arg Leu Arg Lys Ala Leu
770 775 780

Leu Asp Gly Arg Ser Trp Asn Pro Glu Glu Gln
 785 790 795

<210> 22
<211> 2427
<212> DNA
<213> Pan troglodytes

<400> 22	
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tatagcttct tcagttccc agaactgcag gtgctggatt tatccaggtg taaaatccag	180
acaattgaag atggggcata tcagagccta agccacctct ccaccttaat attgacagga	240
aaccccatcc agagtttagc cctgggagcc tttctggac tatcaagttt acagaagctg	300
gtggctgtgg agacaaatct agcatctcta gagaacttcc ccattggaca tctaaaaact	360
ttgaaagaac ttaatgtggc tcacaatctt atccaatctt tcaaattacc tgagtatTTT	420
tctaattctga ccaatctaga gcacttggac ctttccagca acaagattca aagtatttt	480
tgcacagact tgcgggttct acatcaaatg cccctactca atctctctt agacctgtcc	540
ctgaacccta tgaactttat ccaaccaggc gcatttaaag aaatttaggct tcataagctg	600
actttgagaa ataattttga tagtttaaat gtaatgaaaa cttgtattca aggtctggct	660
ggtttagaag tccatcgTTT gttctggga gaatttagaa atgaagaaaa cttggaaaag	720
tttgacaaat ctgctctaga ggcctgtgc aatttgcatt ttgaagaatt ccgattagca	780
tacttagact actaccccgaa tgatattatt gacttattta attgtttgac aaatgtttct	840
tcattttccc tggtgagtgt gactattaa agcgtaaaag actttctta taatttcgga	900
tggcaacatt tagaatttagt taagtgtaaa tttggacagt ttcccacatt gaaactcaaa	960
tctctcaaaa ggcttacttt cacttccaaac aaagggtggga atgcttttc agaagttgat	1020
ctaccaagcc ttgagtttct agatctcagt agaaatggct tgagttcaa aggttgctgt	1080
tctcaaagtg attttggac aaccagccta aagtatttag atctgagctt caatgggttt	1140
attaccatga gttcaaactt cttggctta gaacaactag aacatctgga tttccagcat	1200
tccaatttga aacaaatgag tgagtttca gtattcctat cactcagaaa cctcatttac	1260
cttgacattt ctcatactca caccagaggc gcttcaatg gcatcttcaa tggcttgc	1320
agtctcgaaag tcttggaaaat ggctggcaat tcttccagg aaaacttcc tccagatatc	1380
ttcacagagc tgagaaactt gacccctcg gacctcttc agtgtcaact ggagcagttg	1440

tctccaacag catttaactc actctccagt cttaggtac taaatatgag ccacaacaac	1500
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agtctcaatc acataatgac ttccaaaaaa caggaactac agcatttcc aagtagtcta	1620
gctttcttaa atcttactca gaatgacttt gcttgtactt gtgaacacca aagttcctg	1680
caatggatca aggaccagag gcagctctg gtgaaagttg aacgaatgga atgtgcaaca	1740
ccttcagata agcaggcat gcctgtgctg agttgaata tcacctgtca gatgaataag	1800
accatcattg gtgtgtcggt cctcagtgtg ctgttagtat ctgttgtagc agttctggc	1860
tataagttct attttcacct gatgcttctt gctggctgca taaagtatgg tagaggtgaa	1920
aacatctatg atgccttgt tatctactca agccaggatg aggactgggt aaggaatgag	1980
ctagtaaaga atttagaaga aggggtgcct ccatttcagc tctgccttca ctacagagac	2040
tttattcccg gtgtggccat tgctgccaac atcatccatg aaggttcca taaaagccga	2100
aaggtgattg ttgtgggtgc ccagcacttc atccagagcc gctgggttat ctttgaatat	2160
gagattgctc agacgtggca gtttctgagc agtcgtgctg gtatcatctt cattgtcctg	2220
cagaaggtgg agaagaccct gtcaggcgg caggtggagc tgtaccgcct tctyagcagg	2280
aacacttacc tggagtggga ggacagtgtc ctggggcggc acatcttctg gagacgactc	2340
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<210> 23
<211> 2427
<212> DNA
<213> Pan troglodytes

<220>
<221> CDS
<222> (1)..(2427)

gtg gtt cct aat att act tat caa tgc atg gag ctg aat ttc tac aaa	48
Val Val Pro Asn Ile Thr Tyr Gln Cys Met Glu Leu Asn Phe Tyr Lys	
1 5 10 15	

atc ccc gac aac ctc ccc ttc tca acc aag aac ctg gac ctg agc ttt	96
Ile Pro Asp Asn Leu Pro Phe Ser Thr Lys Asn Leu Asp Leu Ser Phe	
20 25 30	

aat ccc ctg agg cat tta ggc agc tat agc ttc ttc agt ttc cca gaa	144
Asn Pro Leu Arg His Leu Gly Ser Tyr Ser Phe Phe Ser Phe Pro Glu	
35 40 45	

cgg cag gtg ctg gat tta tcc agg tgt gaa atc cag aca att gaa gat	192
Leu Gln Val Leu Asp Leu Ser Arg Cys Glu Ile Gln Thr Ile Glu Asp	

50	55	60	
ggg gca tat cag agc cta agc cac ctc tcc acc tta ata ttg aca gga Gly Ala Tyr Gln Ser Leu Ser His Leu Ser Thr Leu Ile Leu Thr Gly	65	70	240
aac ccc atc cag agt tta gcc ctg gga gcc ttt tct gga cta tca agt Asn Pro Ile Gln Ser Leu Ala Leu Gly Ala Phe Ser Gly Leu Ser Ser	85	90	288
tta cag aag ctg gtg gct gtg gag aca aat cta gca tct cta gag aac Leu Gln Lys Leu Val Ala Val Glu Thr Asn Leu Ala Ser Leu Glu Asn	100	105	336
ttc ccc att gga cat ctc aaa act ttg aaa gaa ctt aat gtg gct cac Phe Pro Ile Gly His Leu Lys Thr Leu Lys Glu Leu Asn Val Ala His	115	120	384
aat ctt atc caa tct ttc aaa tta cct gag tat ttt tct aat ctg acc Asn Leu Ile Gln Ser Phe Lys Leu Pro Glu Tyr Phe Ser Asn Leu Thr	130	135	432
aat cta gag cac ttg gac ctt tcc agc aac aag att caa agt att tat Asn Leu Glu His Leu Asp Leu Ser Ser Asn Lys Ile Gln Ser Ile Tyr	145	150	480
tgc aca gac ttg cggtt cta cat caa atg ccc cta ctc aat ctc tct Cys Thr Asp Leu Arg Val Leu His Gln Met Pro Leu Leu Asn Leu Ser	165	170	528
tta gac ctg tcc ctg aac cct atg aac ttt atc caa cca ggt gca ttt Leu Asp Leu Ser Leu Asn Pro Met Asn Phe Ile Gln Pro Gly Ala Phe	180	185	576
aaa gaa att agg ctt cat aag ctg act ttg aga aat aat ttt gat agt Lys Glu Ile Arg Leu His Lys Leu Thr Leu Arg Asn Asn Phe Asp Ser	195	200	624
tta aat gta atg aaa act tgt att caa ggt ctg gct ggt tta gaa gtc Leu Asn Val Met Lys Thr Cys Ile Gln Gly Leu Ala Gly Leu Glu Val	210	215	672
cat cgt ttg gtt ctg gga gaa ttt aga aat gaa gaa aac ttg gaa aag His Arg Leu Val Leu Gly Glu Phe Arg Asn Glu Glu Asn Leu Glu Lys	225	230	720
ttt gac aaa tct gct cta gag ggc ctg tgc aat ttg acc att gaa gaa Phe Asp Lys Ser Ala Leu Glu Gly Leu Cys Asn Leu Thr Ile Glu Glu	245	250	768
ttc cga tta gca tac tta gac tac tac ctc gat gat att att gac tta Phe Arg Leu Ala Tyr Leu Asp Tyr Tyr Leu Asp Asp Ile Ile Asp Leu	260	265	816
ttt aat tgt ttg aca aat gtt tct tca ttt tcc ctg gtg agt gtg act Phe Asn Cys Leu Thr Asn Val Ser Ser Phe Ser Leu Val Ser Val Thr	275	280	864
att aaa agc gta aaa gac ttt tct tat aat ttc gga tgg caa cat tta Ile Lys Ser Val Lys Asp Phe Ser Tyr Asn Phe Gly Trp Gln His Leu			912

290	295	300	
gaa tta gtt aag tgt aaa ttt gga cag ttt ccc aca ttg aaa ctc aaa Glu Leu Val Lys Cys Lys Phe Gly Gln Phe Pro Thr Leu Lys Leu Lys 305 310 315 320			960
tct ctc aaa agg ctt act ttc act tcc aac aaa ggt ggg aat gct ttt Ser Leu Lys Arg Leu Thr Phe Thr Ser Asn Lys Gly Gly Asn Ala Phe 325 330 335			1008
tca gaa gtt gat cta cca agc ctt gag ttt cta gat ctc agt aga aat Ser Glu Val Asp Leu Pro Ser Leu Glu Phe Leu Asp Leu Ser Arg Asn 340 345 350			1056
ggc ttg agt ttc aaa ggt tgc tgc tct caa agt gat ttt ggg aca acc Gly Leu Ser Phe Lys Gly Cys Cys Ser Gln Ser Asp Phe Gly Thr Thr 355 360 365			1104
agc cta aag tat tta gat ctg agc ttc aat ggt gtt att acc atg agt Ser Leu Lys Tyr Leu Asp Leu Ser Phe Asn Gly Val Ile Thr Met Ser 370 375 380			1152
tca aac ttc ttg ggc tta gaa caa cta gaa cat ctg gat ttc cag cat Ser Asn Phe Leu Gly Leu Glu Gln Leu Glu His Leu Asp Phe Gln His 385 390 395 400			1200
tcc aat ttg aaa caa atg agt gag ttt tca gta ttc cta tca ctc aga Ser Asn Leu Lys Gln Met Ser Glu Phe Ser Val Phe Leu Ser Leu Arg 405 410 415			1248
aac ctc att tac ctt gac att tct cat act cac acc aga gtt gct ttc Asn Leu Ile Tyr Leu Asp Ile Ser His Thr His Thr Arg Val Ala Phe 420 425 430			1296
aat ggc atc ttc aat ggc ttg tcc agt ctc gaa gtc ttg aaa atg gct Asn Gly Ile Phe Asn Gly Leu Ser Ser Leu Glu Val Leu Lys Met Ala 435 440 445			1344
ggc aat tct ttc cag gaa aac ttc ctt cca gat atc ttc aca gag ctg Gly Asn Ser Phe Gln Glu Asn Phe Leu Pro Asp Ile Phe Thr Glu Leu 450 455 460			1392
aga aac ttg acc ttc ctg gac ctc tct cag tgt caa ctg gag cag ttg Arg Asn Leu Thr Phe Leu Asp Leu Ser Gln Cys Gln Leu Glu Gln Leu 465 470 475 480			1440
tct cca aca gca ttt aac tca ctc tcc agt ctt cag gta cta aat atg Ser Pro Thr Ala Phe Asn Ser Leu Ser Leu Gln Val Leu Asn Met 485 490 495			1488
agc cac aac aac ttc ttt tca ttg gat acg ttt cct tat aag tgt ctg Ser His Asn Asn Phe Phe Ser Leu Asp Thr Phe Pro Tyr Lys Cys Leu 500 505 510			1536
aac tcc ctc cag gtt ctt gat tac agt ctc aat cac ata atg act tcc Asn Ser Leu Gln Val Leu Asp Tyr Ser Leu Asn His Ile Met Thr Ser 515 520 525			1584
aaa aaa cag gaa cta cag cat ttt cca agt agt cta gct ttc tta aat Lys Lys Gln Glu Leu Gln His Phe Pro Ser Ser Leu Ala Phe Leu Asn			1632

530	535	540	
ctt act cag aat gac ttt gct tgt act tgt gaa cac caa agt ttc ctg Leu Thr Gln Asn Asp Phe Ala Cys Thr Cys Glu His Gln Ser Phe Leu 545 550 555 560			1680
caa tgg atc aag gac cag agg cag ctc ttg gtg gaa gtt gaa cga atg Gln Trp Ile Lys Asp Gln Arg Gln Leu Leu Val Glu Val Glu Arg Met 565 570 575			1728
gaa tgt gca aca cct tca gat aag cag ggc atg cct gtg ctg agt ttg Glu Cys Ala Thr Pro Ser Asp Lys Gln Gly Met Pro Val Leu Ser Leu 580 585 590			1776
aat atc acc tgt cag atg aat aag acc atc att ggt gtg tcg gtc ctc Asn Ile Thr Cys Gln Met Asn Lys Thr Ile Ile Gly Val Ser Val Leu 595 600 605			1824
agt gtg ctt gta gta tct gtt gta gca gtt ctg gtc tat aag ttc tat Ser Val Leu Val Val Ser Val Val Ala Val Leu Val Tyr Lys Phe Tyr 610 615 620			1872
ttt cac ctg atg ctt ctt gct ggc tgc ata aag tat ggt aga ggt gaa Phe His Leu Met Leu Leu Ala Gly Cys Ile Lys Tyr Gly Arg Gly Glu 625 630 635 640			1920
aac atc tat gat gcc ttt gtt atc tac tca agc cag gat gag gac tgg Asn Ile Tyr Asp Ala Phe Val Ile Tyr Ser Ser Gln Asp Glu Asp Trp 645 650 655			1968
gta agg aat gag cta gta aag aat tta gaa gaa ggg gtg cct cca ttt Val Arg Asn Glu Leu Val Lys Asn Leu Glu Glu Gly Val Pro Pro Phe 660 665 670			2016
cag ctc tgc ctt cac tac aga gac ttt att ccc ggt gtg gcc att gct Gln Leu Cys Leu His Tyr Arg Asp Phe Ile Pro Gly Val Ala Ile Ala 675 680 685			2064
gcc aac atc atc cat gaa ggt ttc cat aaa agc cga aag gtg att gtt Ala Asn Ile Ile His Glu Gly Phe His Lys Ser Arg Lys Val Ile Val 690 695 700			2112
gtg gtg tcc cag cac ttc atc cag agc cgc tgg tgt atc ttt gaa tat Val Val Ser Gln His Phe Ile Gln Ser Arg Trp Cys Ile Phe Glu Tyr 705 710 715 720			2160
gag att gct cag acg tgg cag ttt ctg agc agt cgt gct ggt atc atc Glu Ile Ala Gln Thr Trp Gln Phe Leu Ser Ser Arg Ala Gly Ile Ile 725 730 735			2208
ttc att gtc ctg cag aag gtg gag aag acc ctg ctc agg cgg cag gtg Phe Ile Val Leu Gln Lys Val Glu Lys Thr Leu Leu Arg Arg Gln Val 740 745 750			2256
gag ctg tac cgc ctt cty agc agg aac act tac ctg gag tgg gag gac Glu Leu Tyr Arg Leu Xaa Ser Arg Asn Thr Tyr Leu Glu Trp Glu Asp 755 760 765			2304
agt gtc ctg ggg cgg cac atc ttc tgg aga cga ctc aga aaa gcc ctg Ser Val Leu Gly Arg His Ile Phe Trp Arg Arg Leu Arg Lys Ala Leu			2352

770

775

780

ctg gat ggt aaa tca tgg aat cca gaa gga aca gtg ggt aca gga tgc 2400
 Leu Asp Gly Lys Ser Trp Asn Pro Glu Gly Thr Val Gly Thr Gly Cys
 785 790 795 800

aat tgg cag gaa gca aca tct atc tga 2427
 Asn Trp Gln Glu Ala Thr Ser Ile
 805

<210> 24
 <211> 808
 <212> PRT
 <213> Pan troglodytes

<220>
 <221> misc_feature
 <222> (758)..(758)
 <223> The 'Xaa' at location 758 stands for Leu.

<400> 24

Val Val Pro Asn Ile Thr Tyr Gln Cys Met Glu Leu Asn Phe Tyr Lys
 1 5 10 15

Ile Pro Asp Asn Leu Pro Phe Ser Thr Lys Asn Leu Asp Leu Ser Phe
 20 25 30

Asn Pro Leu Arg His Leu Gly Ser Tyr Ser Phe Phe Ser Phe Pro Glu
 35 40 45

Leu Gln Val Leu Asp Leu Ser Arg Cys Glu Ile Gln Thr Ile Glu Asp
 50 55 60

Gly Ala Tyr Gln Ser Leu Ser His Leu Ser Thr Leu Ile Leu Thr Gly
 65 70 75 80

Asn Pro Ile Gln Ser Leu Ala Leu Gly Ala Phe Ser Gly Leu Ser Ser
 85 90 95

Leu Gln Lys Leu Val Ala Val Glu Thr Asn Leu Ala Ser Leu Glu Asn
 100 105 110

Phe Pro Ile Gly His Leu Lys Thr Leu Lys Glu Leu Asn Val Ala His
 115 120 125

Asn Leu Ile Gln Ser Phe Lys Leu Pro Glu Tyr Phe Ser Asn Leu Thr
 130 135 140

Asn Leu Glu His Leu Asp Leu Ser Ser Asn Lys Ile Gln Ser Ile Tyr

145

150

155

160

Cys Thr Asp Leu Arg Val Leu His Gln Met Pro Leu Leu Asn Leu Ser
165 170 175

Leu Asp Leu Ser Leu Asn Pro Met Asn Phe Ile Gln Pro Gly Ala Phe
180 185 190

Lys Glu Ile Arg Leu His Lys Leu Thr Leu Arg Asn Asn Phe Asp Ser
195 200 205

Leu Asn Val Met Lys Thr Cys Ile Gln Gly Leu Ala Gly Leu Glu Val
210 215 220

His Arg Leu Val Leu Gly Glu Phe Arg Asn Glu Glu Asn Leu Glu Lys
225 230 235 240

Phe Asp Lys Ser Ala Leu Glu Gly Leu Cys Asn Leu Thr Ile Glu Glu
245 250 255

Phe Arg Leu Ala Tyr Leu Asp Tyr Tyr Leu Asp Asp Ile Ile Asp Leu
260 265 270

Phe Asn Cys Leu Thr Asn Val Ser Ser Phe Ser Leu Val Ser Val Thr
275 280 285

Ile Lys Ser Val Lys Asp Phe Ser Tyr Asn Phe Gly Trp Gln His Leu
290 295 300

Glu Leu Val Lys Cys Lys Phe Gly Gln Phe Pro Thr Leu Lys Leu Lys
305 310 315 320

Ser Leu Lys Arg Leu Thr Phe Thr Ser Asn Lys Gly Gly Asn Ala Phe
325 330 335

Ser Glu Val Asp Leu Pro Ser Leu Glu Phe Leu Asp Leu Ser Arg Asn
340 345 350

Gly Leu Ser Phe Lys Gly Cys Cys Ser Gln Ser Asp Phe Gly Thr Thr
355 360 365

Ser Leu Lys Tyr Leu Asp Leu Ser Phe Asn Gly Val Ile Thr Met Ser
370 375 380

Ser Asn Phe Leu Gly Leu Glu Gln Leu Glu His Leu Asp Phe Gln His

385

390

395

400

Ser Asn Leu Lys Gln Met Ser Glu Phe Ser Val Phe Leu Ser Leu Arg
405 410 415

Asn Leu Ile Tyr Leu Asp Ile Ser His Thr His Thr Arg Val Ala Phe
420 425 430

Asn Gly Ile Phe Asn Gly Leu Ser Ser Leu Glu Val Leu Lys Met Ala
435 440 445

Gly Asn Ser Phe Gln Glu Asn Phe Leu Pro Asp Ile Phe Thr Glu Leu
450 455 460

Arg Asn Leu Thr Phe Leu Asp Leu Ser Gln Cys Gln Leu Glu Gln Leu
465 470 475 480

Ser Pro Thr Ala Phe Asn Ser Leu Ser Ser Leu Gln Val Leu Asn Met
485 490 495

Ser His Asn Asn Phe Phe Ser Leu Asp Thr Phe Pro Tyr Lys Cys Leu
500 505 510

Asn Ser Leu Gln Val Leu Asp Tyr Ser Leu Asn His Ile Met Thr Ser
515 520 525

Lys Lys Gln Glu Leu Gln His Phe Pro Ser Ser Leu Ala Phe Leu Asn
530 535 540

Leu Thr Gln Asn Asp Phe Ala Cys Thr Cys Glu His Gln Ser Phe Leu
545 550 555 560

Gln Trp Ile Lys Asp Gln Arg Gln Leu Leu Val Glu Val Glu Arg Met
565 570 575

Glu Cys Ala Thr Pro Ser Asp Lys Gln Gly Met Pro Val Leu Ser Leu
580 585 590

Asn Ile Thr Cys Gln Met Asn Lys Thr Ile Ile Gly Val Ser Val Leu
595 600 605

Ser Val Leu Val Val Ser Val Val Ala Val Leu Val Tyr Lys Phe Tyr
610 615 620

Phe His Leu Met Leu Leu Ala Gly Cys Ile Lys Tyr Gly Arg Gly Glu

625

630

635

640

Asn Ile Tyr Asp Ala Phe Val Ile Tyr Ser Ser Gln Asp Glu Asp Trp
645 650 655

Val Arg Asn Glu Leu Val Lys Asn Leu Glu Glu Gly Val Pro Pro Phe
660 665 670

Gln Leu Cys Leu His Tyr Arg Asp Phe Ile Pro Gly Val Ala Ile Ala
675 680 685

Ala Asn Ile Ile His Glu Gly Phe His Lys Ser Arg Lys Val Ile Val
690 695 700

Val Val Ser Gln His Phe Ile Gln Ser Arg Trp Cys Ile Phe Glu Tyr
705 710 715 720

Glu Ile Ala Gln Thr Trp Gln Phe Leu Ser Ser Arg Ala Gly Ile Ile
725 730 735

Phe Ile Val Leu Gln Lys Val Glu Lys Thr Leu Leu Arg Arg Gln Val
740 745 750

Glu Leu Tyr Arg Leu Xaa Ser Arg Asn Thr Tyr Leu Glu Trp Glu Asp
755 760 765

Ser Val Leu Gly Arg His Ile Phe Trp Arg Arg Leu Arg Lys Ala Leu
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Leu Asp Gly Lys Ser Trp Asn Pro Glu Gly Thr Val Gly Thr Gly Cys
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Asn Trp Gln Glu Ala Thr Ser Ile
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Phe Ser Leu
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Ser Ser Lys Asp Ser Ile Asp Leu Leu Asn Cys Leu Ala Asp Ile Ser
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Lys Ile Ser Leu
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Ser Leu